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A
JC930 U.S. PTO
09/77450
11/20/00

Docket No. 0630/PD532 US1

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Lisa Ann NEUHOLD and Loren KILLAR

For: TRANSGENIC ANIMAL MODEL FOR DEGENERATIVE DISEASE OF
CARTILAGE

CONTINUING APPLICATION

Hon. Commissioner of
Patents and Trademarks
Washington, DC 20231

Sir:

This is a request for filing under 37 C.F.R. 1.53(b) of a:

☒ Continuation ☐ Divisional

application of the following pending prior application:

Serial No. 08/994,689 Filed: 12/19/97

Of: NEUHOLD et al.

For: TRANSGENIC ANIMAL MODEL FOR DEGENERATIVE DISEASE OF
CARTILAGE

Examiner: M. Wilson Group: 1633

1. Enclosed is a copy of the prior application as originally filed (along with a copy of the original Declaration). No amendments identified in the

09/77450 11/20/00

A vertical strip of seven small, square, black-and-white photographs showing the progression of a plant's growth from a seedling to a mature plant. The images are arranged vertically, with the seedling at the top and the mature plant at the bottom. The plants are shown in various stages of development, from a small seedling to a mature plant with a large, rounded head.

- | CLAIMS AS FILED, AFTER ACCOMPANYING AMENDMENT | | | |
|---|-------------------|--------------|----------|
| | Claims on
File | Number Extra | Rate |
| Basic Fee | | | \$710.00 |
| Total Claims | 27- 20 = | x \$ | \$126.00 |
| Independent Claims | 2- 3 = | x \$ | \$ |
| If Multiple Dependent Claims Are Present, Add \$.00 | | | \$ |
| Total Filing Fee | | | \$836.00 |
| For Small Entity (half of preceding total)* | | | \$ |

3. A check in the amount of \$836.00 is enclosed.
4. ☐ Cancel claims _.
5. ☒ Amend the specification by inserting before the first line the sentence (check one and fill in):

"This is a ☒ continuation, ☐ division, of application Serial No. 08/994,689, filed 12/19/97. Each prior application is hereby incorporated herein by reference, in its entirety."
6. ☒ The prior application is assigned to: American Home Products Corporation
7. ☒ A Preliminary Amendment is also enclosed.

- 2 -

8. ☒ Informal Drawings are filed herewith
9. ☐ A verified statement claiming small entity status (check one):
☐ was filed in parent application or ☐ is enclosed.
10. ☐ Priority is claimed from
Country:
Number:
Date:

The priority document

- ☐ was filed in the prior application
☐ is enclosed.

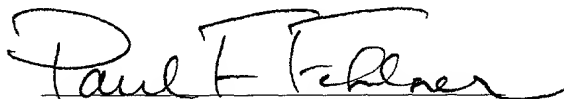
11. The Assignment

- ☒ was recorded at Reel 8934 Frame 0165 on December 19, 1997
☐ is enclosed.

12. Sequence Listing

Pursuant to 37 C.F.R. § 12.82(e), please use the computer readable form (CRF) of the "Sequence Listing" from parent application Serial No. 08/944,689, filed December 19, 1997, in this application. The paper copy of the "Sequence Listing" in this application is identical to CRF filed for the parent application.

Respectfully submitted,



Paul F. Fehlner, Ph.D.

Reg. No. 35,135

Attorney of Record in Prior Application

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Name: _____

Docket No.: 0630/1D532US1

Please add the following claims:

--28. A transgenic non-human mammal or progeny thereof whose somatic and germline cells contain, in stably integrated form,

- (a) a first coding sequence encoding an enzymatically active matrix degrading enzyme (MDE) that degrades an extracellular matrix component, wherein expression of the first coding sequence is under control of a regulatable promoter that is responsive to a transcriptional repressor or activator polypeptide; and
- (b) a second coding sequence encoding the transcriptional repressor or activator polypeptide, wherein expression of the second coding sequence is under control of a chondrocyte tissue-specific promoter;

wherein expression of the MDE by chondrocytes is repressed throughout embryonic, fetal, and early postnatal development, and activation of expression of the MDE results in a phenotypic change characteristic of osteoarthritis.

29. The transgenic mammal of claim 28, wherein the MDE is a matrix metalloproteinase selected from the group consisting of MMP-1, MMP-3, MMP-8, and MMP-13.

30. The transgenic mammal of claim 28, wherein the MDE is constitutively enzymatically active without proteolytic processing.

31. The transgenic mammal of claim 30, wherein the MDE is a constitutively enzymatically active MMP-13 variant.

32. The transgenic mammal of claim 31, wherein the MMP-13 variant has a sequence of ID NO:1 or SEQ ID NO:21.

33. The transgenic mammal of claim 28, wherein the mammal is selected from the group consisting of a mouse, a rat, and a rabbit.

34. The transgenic mammal of claim 28, wherein the mammal is a mouse.

35. The transgenic mammal of claim 28, wherein the transcriptional repressor or activator polypeptide is a repressor polypeptide.

36. The transgenic mammal of claim 35, wherein the repressor polypeptide is a tetracycline repressor polypeptide.

37. The transgenic mammal of claim 36, wherein the regulatable promoter comprises a tet07 sequence.

38. The transgenic mammal of claim 37, wherein the regulatable promoter comprises a sequence depicted in SEQ ID NO:2.

39. The transgenic mammal of claim 28, wherein the chondrocyte tissue-specific promoter comprises sequences from a Type II collagen promoter.

40. The transgenic mammal of claim 28, wherein the phenotypic change characteristic of osteoarthritis is selected from the group consisting of loss of proteoglycan, cleavage of Type II collagen, gross observations of changes in joint function, joint space narrowing, collagen degradation, destruction of cartilage, changes in growth plate morphology, fibrillation and loss of articular cartilage, osteophyte formation, and combinations thereof.

41. A transgenic mouse or rat, or progeny thereof, whose somatic and germline cells contain, in stably integrated form,

- (a) a first coding sequence encoding a constitutively enzymatically active matrix metalloproteinase (MMP) that cleaves Type II collagen, wherein expression of the first coding sequence is under control of a tetracycline-regulatable promoter; and
- (b) a second coding sequence encoding a tetracycline repressor polypeptide that binds to the tetracycline-regulatable promoter, wherein expression of the second coding sequence is under control of a chondrocyte tissue-specific promoter;

wherein expression of the MMP by chondrocytes is repressed throughout embryonic, fetal, and early postnatal development, and activation of expression of the MMP results in a phenotypic change characteristic of osteoarthritis in the transgenic mouse or rat.

42. The transgenic mouse or rat of claim 41, wherein the MMP is constitutively enzymatically active MMP-13, the tetracycline regulatable promoter is a tetO7 promoter, the tetracycline repressor polypeptide is a tTA polypeptide, and the chondrocyte tissue-specific promoter comprises sequences from a Type II collagen promoter.

43. The transgenic mouse or rat of claim 42, wherein the phenotypic change characteristic of osteoarthritis is selected from the group consisting of loss of proteoglycan, cleavage of Type II collagen, gross observations of changes in joint function, joint space narrowing, collagen degradation, destruction of cartilage, changes in growth plate morphology, fibrillation and loss of articular cartilage, osteophyte formation, and combinations thereof.

44. A method for producing a phenotypic change characteristic of osteoarthritis in a transgenic mammal of claim 28, which method comprises activating MDE expression in the transgenic mammal after embryonic, fetal, and early postnatal development.

45. The method according to claim 44, wherein the phenotypic change

characteristic of osteoarthritis is selected from the group consisting of loss of proteoglycan, cleavage of Type II collagen, gross observations of changes in joint function, joint space narrowing, collagen degradation, destruction of cartilage, changes in growth plate morphology, fibrillation and loss of articular cartilage, osteophyte formation, and combinations thereof.

46. A method for producing a phenotypic change characteristic of osteoarthritis in the transgenic mammal of claim 36, which method comprises maintaining the transgenic mammal on tetracycline or a tetracycline analog during embryonic, fetal, and early postnatal development, and activating the MDE expression by withholding the tetracycline or tetracycline analog after embryonic, fetal, and early postnatal development.

47. The method according to claim 46, wherein the tetracycline analog is doxycycline.

48. The method according to claim 46, wherein the phenotypic change characteristic of osteoarthritis is selected from the group consisting of loss of proteoglycan, cleavage of Type II collagen, gross observations of changes in joint function, joint space narrowing, collagen degradation, destruction of cartilage, changes in growth plate morphology, fibrillation and loss of articular cartilage, osteophyte formation, and combinations thereof.

49. A method for producing a phenotypic change characteristic of osteoarthritis in the transgenic mouse or rat of claim 41, which method comprises maintaining the transgenic mouse or rat on tetracycline or a tetracycline analog during embryonic, fetal, and early postnatal development, and activating the collagenase expression by withholding the tetracycline or tetracycline analog after embryonic, fetal, and early postnatal development.

50. The method according to claim 49, wherein the tetracycline analog is doxycycline.

The claims in the application as filed have been canceled and new claims 28-54 have been added to more particularly point out and distinctly claim that which applicants regard as the invention. The new claims are fully supported by the claims as filed and by the specification. In particular, support for new claims 29-55 is set forth in the following table:

<u>New Claims</u>	<u>Support</u>
28.	Claim 1 as filed; p. 27, l. 9 (coding sequence); at p. 2, l. 4 and p. 5, ll. 19-20 (enzymatically active matrix degrading enzyme (MDE) that degrades an extracellular matrix component); p. 6, ll. 11-12 (regulatable promoter); p. 13, ll. 6-8 (promoter that is responsive to a transcriptional repressor or activator polypeptide); p. 37, l. 1, p. 6, ll. 4-5, p. 13, ll. 3-4 (chondrocyte tissue-specific promoter); p. 13, l. 1, p. 16, ll. 12-15 (expression repressed throughout embryonic, fetal, and early postnatal development); p. 6, l. 5-6, p. 18, ll. 9-11 (MDE expression results in a phenotypic change characteristic of osteoarthritis).
29.	p. 2, Table 1 and p. 5, ll. 23-24.
30.	p. 12, l. 8.
31.	p. 12, l. 13.
32.	claim 7 as filed; p. 12, ll. 16-18.
33.	claim 8 as filed.
34.	claim 9 as filed.

35. p. 13, l. 10.
36. p. 14, l. 21.
37. claim 11 as filed; p. 14, ll. 21-22
38. claim 12 as filed
39. claim 15 as filed; p. 16, l. 2.
40. (also 43, 45, 48, and 51) p. 18, ll. 13-15; p. 19, ll. 11-18; p. 21, ll. 5-6.
41. p. 27, l. 9 (coding sequence); p. 12, ll. 8-12 (constitutively active MMP); p.3, ll. 4-5, p. 11, ll. 5-6 (degrades Type II collagen) p. 6, ll. 11-12; p. 13, ll. 6-8 and 19; (tetracycline regulatable promoter); p. 13, l. 19 (tetracycline repressor polypeptide); p. 37, l. 1; p. 6, ll. 4-5; p. 13, ll. 3-4 (chondrocyte tissue-specific promoter); p. 13, l. 1 and p. 16, ll. 12-15 (expression repressed throughout embryonic, fetal, and early postnatal development); p. 18, ll. 9-11 (MMP expression results in phenotypic change characteristic of osteoarthritis).
42. claim 16 as filed; p. 17, l. 24 to p. 18, l. 2.
44. (also 46 and 49) claims 22-24 as filed; p. 18, ll. 16-21.
47. (also 50) p. 41, l. 6.

SUMMARY OF POINTS

Based on the grounds for rejection in the outstanding Final Office Action in the '689 parent application, and the discussion at the interview in the '689 parent application conducted on May 17, 2000, applicants submit that there are no issues with respect to patentability of the specific transgenic mice exemplified in this application. However, as discussed at the interview, such a limited claim scope denies the protection to which this discovery is entitled: any transgenic animal that expresses an enzymatically active matrix degrading enzyme under control of an inducible promoter and a tissue-specific promoter, and, when induced to express the enzymatically active matrix degrading enzyme, develops phenotypic changes characteristic of osteoarthritis. Applicants wish to emphasize the following points in support of patentability of the invention as presently claimed:¹

- Enzymatically active matrix degrading enzymes that degrade extracellular matrix components are well known. Applicants have established this in the file history of the application as follows:
Specification: pages 2-3; pages 11-12.
Additional evidence: Second Neuhold Declaration, paragraph 8.
- Expression of coding sequences under control of regulatable promoters that are responsive to a transcriptional repressor or activator polypeptide in transgenic

¹ Applicants refer herein to the Declaration of Lisa A. Neuhold, Ph.D. Under 37 C.F.R. § 1.132 filed April 6, 1999 (the Neuhold Declaration; copy attached as Exhibit A), the preliminary Amendment filed by hand on February 18, 2000 (the Preliminary Amendment; copy attached as Exhibit B) and the Second Declaration of Lisa A. Neuhold, Ph.D. Under 37 C.F.R. § 1.132 filed August 30, 2000 (the Second Neuhold Declaration; copy attached as Exhibit C), filed in the '689 parent application.

animals is well known. Applicants have established this in the file history of this application as follows:

Specification: pages 12-15 and pages 16-18.

Additional Evidence: Exhibits A, B, C, D, and E to

Preliminary Amendment; Second Neuhold

Declaration, paragraph 6.

- Tissue specific expression of transgenes in transgenic animals is well known. Applicants have established this in the file history of this application as follows:

Specification: pages 15-16 and 17-18.

Additional Evidence: Neuhold Declaration,

paragraph 6; Second Neuhold Declaration,

paragraph 7 and Tab 2.

- Transgenic nonhuman mammals, particularly mice, rats, and rabbits, are well known and prepared routinely by ordinary research scientists at the time this invention was made. It is also a known and accepted that, as with every other experimental system in biology such as cloning and hydridomas, not every transgenic embryo will yield a transgenic animal with the desired characteristics, but that routine screening and selection techniques will provide such an animal as claimed. Applicants have established this extensively in the file history of this application as follows:

Specification: pages 22-26.

Additional Evidence: Second Neuhold Declaration,

paragraph 9 and Tab 4.

The Examiner also contended that the specification does not teach how to get other phenotypes. Applicants disagree; the record as set forth above and the Second Neuhold Declaration (paragraphs 10 and 11) firmly establishes that the transgenic mammals, and especially rodents, of the invention, upon expression of the matrix degrading enzyme, develops a phenotypic change characteristic of osteoarthritis.

The Examiner contended that it is not clear whether other extracellular matrix degrading enzymes would achieve the claimed phenotype. Applicants respectfully disagree. The specification sets forth a plethora of matrix degrading enzymes (pages 2-3); the Examiner has provided no evidence or documentation to substantiate doubts that other MDEs would achieve this phenotype. It is uncontroverted that other Type II collagenase enzymes, such as MMP-1, MMP-8, and MMP-13, would (see claim 41). The Examiner has the burden to establish a reasonable basis to question the enablement provided for the claimed invention. *In re Wright*, 27 USPQ2d 1510 (Fed. Cir. 1993). MPEP § 2164.04. The Examiner clearly failed to meet this burden here.⁴ In contrast, Applicants have more than met theirs: in addition to the express disclosure of the specification (see pages 2-3 and 11-12), they have further addressed this issue in the interview and by Rule 132 Declaration (*see* the Second Neuhold Declaration, paragraph 8). Thus, this rejection is overcome and should be withdrawn. Claim 41 particularly addresses these concerns by reciting a constitutively active collagen II-specific MMP.

The Examiner asserted that the invention is unpredictable with regard to phenotype. However, the evidence of record in the specification (pages 41-44), the Neuhold Declaration (paragraphs 9, 11, 13, 14, and 15), and the Second Neuhold Declaration (paragraphs 10 and 11) firmly establish that the transgenic animals of the invention demonstrate the claimed phenotypic change, *i.e.*, one or more characteristics of osteoarthritis.

⁴ The '689 Final Office Action does not address this defect.

The Examiner also asserted that non-mutated MMP genes are not enabled. As these proteins, and methods for activating them, are extremely well known in the art (as agreed at the interview), which is specifically established on pages 2-3 of the specification, Applicants submit that this rejection is obviated and should be withdrawn. Furthermore, this rejection does not properly apply to claim 41.

The Examiner further contended that the specification is only enabled for MMP13* and exemplified phenotype. For the reasons set forth above, Applicants submit that the specification broadly enables transgenic mammals that express any MDE in a tissue specific, temporally regulated fashion. Furthermore, as the exemplified phenotype is a phenotypic change characteristic of osteoarthritis, which includes cartilage degradation (Second Neuhold Declaration, paragraphs 10 and 11), the specification clearly enables this aspect of the claimed invention as well. Thus, these bases for rejecting the claims are obviated and should be withdrawn.

The Examiner contended that the specification is not enabled for any joint specific promoter and should recite only a Type II collagen promoter. As discussed during the interview and set forth in the Second Neuhold Declaration (paragraph 7), the specific promoter employed to achieve tissue specific expression does not make any difference, as one of ordinary skill in the art would readily appreciate. A number of issued patents that cover transgenic animals establish tissue-specific expression is sufficiently enabled for expression of a transgene, because the actual tissue specific promoter is usually of no moment. Moreover, it is proper in a patent for a transgenic animal to claim the promoter by virtue of its tissue specificity rather than identity. *See* U.S. Patent Nos. 5,625,124 (claim 1: "gut epithelial cell specific promoter"); 5,880,327 (claim 1: "a mammary-gland specific promoter"); 5,917,123 (claim 1: "a cardiac-specific regulatory region"); 6,028,245 (claim 1: "a promoter that drives expression of the transgene in skin")

(attached as Exhibit 2). In view of the foregoing, the Examiner's basis for this rejection is obviated and should be withdrawn.⁵

The Examiner cited references detailing expression in other mammals as support for argument that the specification does not enable non-human mammals besides mouse. Applicants respectfully take issue with these citations on two grounds. First, they support the opposite conclusion: that the claimed transgenic animals are enabled. Second, these references do not adequately support the rejection. Applicants submit that the Examiner has not carried this burden where the support (1) generally refers to the generic technology; (2) addresses questions related to economics and commercialization, not § 112, first paragraph; (3) contains no information specifically relevant to the claimed invention; and (4) is out of date (none of the references cited by the Examiner have publication dates later than 1996; one was published in 1988; in a rapidly evolving field such as transgenic animals, only the most current references from the time the invention was made have any bearing). *Cf. In re Goodman*, 29 USPQ2d 2010 (Fed. Cir. 1993) (applying references directly addressing the claims in issue to establish lack of enablement).⁶

In particular, the Wall reference reports that 6000 papers describe transgenic animals, mostly mice, to answer research questions (pages 58, 60, and 61). Wall states that "... genes can ... be modified to function very differently than they do in their native form (gene products, tissue specificity, and timing of expression can be altered)" (page 58). In other words, Wall specifically states that the features of Applicants' invention can be achieved. Wall does concede that transgenic farm animals are costly (mostly because it takes many attempts to yield the desired transgenic animal) (see page 60), however, economic issues are irrelevant to

⁵ The '689 Final Office Action fails to address any of these issues.

⁶ The '689 Final Office Action does not address any of these issues, or Applicants' contention that the references clearly support enablement, as discussed further.

achieves the desired transgenic animals. Indeed, applicants themselves had failures, among which successful animals were obtained (see page 43 of the specification).

In short, the Examiner's grounds for rejection are in error given the advanced state of the art, including general recognition of enablement of transgenic animals (irrespective of whether or not they are cost effective), widespread knowledge of regulatable expression systems, the understanding in the art of tissue-specific expression, and the number of well known extracellular matrix degrading enzymes from which to choose. The present invention is broadly enabled, and the Examiner has not met his burden of challenging enablement with reasonable evidence. Accordingly, the rejection under 35 U.S.C. § 112, first paragraph is in error and should be withdrawn.

CONCLUSION

Because the claims of this application, which is a continuing application of the '689 application, are drawn to the same invention claimed in the earlier application and would have been properly [sic, procedurally]⁷ finally rejection on the grounds of record in the next Office Action if they had been entered in the '689 application. Accordingly, a Final Rejection is appropriate as a First Office Action in this Continuation application. MPEP § 706.07(b) (Rev. 1, Feb. 2000). Accordingly, if the Examiner persists in rejecting these claims, applicants believe a Final Rejection is appropriate and necessary to permit appeal.

Applicants respectfully request entry of the foregoing amendments and remarks as well as the amendments and Rule 132 Declarations from the '689 application in the file history of this application. In view of the foregoing amendments and remarks, applicants submit that the

⁷ Applicants use the term properly in a procedural context, and do not agree with or concede the rejections in '689.

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	0.45	0.50	0	1
Marital status	0.65	0.48	0	1
Education	12.5	2.5	9	16
Income	2500	1500	500	6000
Health status	0.75	0.42	0	1
Employment	0.85	0.35	0	1
Stress level	4.5	1.5	1	7
Life satisfaction	5.5	1.2	3	7
Depression	0.35	0.48	0	1
Loneliness	0.45	0.50	0	1
Quality of life	6.5	1.5	4	8
Physical health	0.85	0.35	0	1
Mental health	0.75	0.42	0	1
Social support	0.65	0.48	0	1
Resilience	0.55	0.50	0	1
Optimism	0.65	0.48	0	1
Gratitude	0.55	0.50	0	1
Forgiveness	0.45	0.50	0	1
Self-esteem	0.65	0.48	0	1
Life purpose	0.55	0.50	0	1
Meaning in life	0.65	0.48	0	1
Existential well-being	0.55	0.50	0	1
Transcendental well-being	0.45	0.50	0	1
Overall well-being	0.55	0.50	0	1

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G. KARASZI gkaraszi
Name (Print) Signature

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Name (Print) D. Beck Signature D. Beck

**TRANSGENIC ANIMAL MODEL FOR DEGENERATIVE DISEASES OF
CARTILAGE**

Field of the Invention

The present invention pertains to transgenic mammals that express recombinant matrix-degrading enzymes in a temporally and spatially regulated manner. The invention further pertains to model systems incorporating such transgenic mammals for studying degenerative joint diseases, including systems for identifying therapeutic agents and treatment regimens.

Background of the Invention

20 Degenerative diseases of cartilage, including joint and disc diseases such as osteoarthritis, rheumatoid arthritis, and osteochondrodysplasias, are widespread, particularly in the elderly. Early symptoms common to these diseases include progressive loss of proteoglycans in the joint (as evidenced by loss of metachromasia); collagen degradation; fibrillation of the cartilage surface; and, ultimately, loss of cartilage (which is evidenced radiologically as joint space narrowing).

One of the primary targets affected by these diseases is type II collagen, the major structural collagen found in articular cartilage. There is a balance between the

10 15

production of type II collagen and catabolic enzymes that degrade type II collagen during normal remodeling of cartilage and bone. Pathological conditions such as, e.g., degenerative joint diseases, may result when this balance is disrupted.

Among the enzymes that degrade extracellular matrix components are matrix

5 metalloproteinases (MMPs), a family of zinc-dependent enzymes, and aggrecanase (Table 1).

Table 1

Matrix-Degrading Enzymes							
	SUBSTRATES						
	<i>Collagen</i>	<i>Gelatin</i>	<i>Proteoglycan</i>	<i>Fibronectin</i>	<i>Laminin</i>	<i>Elastin</i>	<i>Other</i>
I. Metalloproteinases							
Collagenases							
MMP-1 (intestinal collagenase)	I, II, III, VII, X	✓					
MMP-8 (neutrophil collagenase)	I, II, III						
MMP-13 (collagenase 3)	I, II, III	✓					
Gelatinases							
MMP-2 (gelatinase A)	IV, V, VII, XI	✓		✓	✓	✓	
MMP-9 (gelatinase B)	IV, V	✓	✓				
Stromelysins							
MMP-3 (stromelysin 1)		✓	✓	✓	✓		activates MMP zymogens
MMP-7 (matrilysin)	IV	✓	✓	✓	✓	✓	
MMP-10 (stromelysin 2)	IV, V, IX		✓	✓	✓		activates MMP zymogens
MMP-11 (stromelysin 3)	IV			✓	✓		activates serpins

Matrix-Degrading Enzymes							
	SUBSTRATES						
	<i>Collagen</i>	<i>Gelatin</i>	<i>Proteoglycan</i>	<i>Fibronectin</i>	<i>Laminin</i>	<i>Elastin</i>	<i>Other</i>
Other							
MMP-12 (metalloelastase)						✓	
MMP-14		✓					proMMP-2, proMMP-13
MMP-15							
MMP-16							proMMP-2
MMP-17							
II. Aggrecanase			✓				

MMPs are synthesized in articulating joints by chondrocytes, which, in mature articular cartilage, are terminally differentiated cells that maintain the cartilage-specific matrix phenotype. Overexpression of MMPs relative to endogenous MMP inhibitors, as occurs in degenerative joint diseases, may result in cartilage degradation. For example, Type II collagen is a substrate for MMP-13 and MMP-1 (Knauper et al., *J. Biol. Chem.* **271**:1544, 1996) and both MMP-1 and MMP-13 proteins can be detected immunohistochemically in human osteoarthritic tissues. In some cases, MMP-13 and its cleavage products are found at higher levels than MMP-1. Billingham et al., *J. Clin. Inves.* **99**:1534, 1997. Thus, MMP-13 may play an important role in cartilage degradation associated with osteoarthritis and other degenerative joint diseases. (Mitchell et al., *J. Clin. Inves.* **97**:761, 1996).

Animal models for osteoarthritis-related syndromes have been described in guinea pigs (Watson et al., *Arth. Rheum.* **39**:1327, 1996) and in the inbred STR/ORT strain

of mice (Das-Gupta et al., *Int. J. Exp. Path.* **74**:627, 1993). In guinea pigs, spontaneous osteoarthritis has a long course of development (six months or more), and only certain sublines of STR/ORT mice consistently develop degenerative joint disease. Thus, the duration and/or variability of these models renders them less applicable to drug discovery studies.

Other osteoarthritis-related models include surgically-induced joint destabilization, e.g., anterior cruciate ligament transection and/or partial meniscectomy in rabbits and dogs, which stimulates cartilage degradation. Hulth et al., *Acta Orthop. Scand.* **41**:522, 1970. Another model employs injection of bacterial collagenase into the joints of an animal to induce a biochemical ligament transection. Van der Kraan et al., *J. Exp. Pathol.* **71**:19, 1990. Because (i) surgical or other manipulation of individual animals is required; (ii) the animals are large and expensive; and/or (iii) the course of disease is not consistent, these models cannot easily be used in large-scale studies, including drug screening.

Transgenic animal models, in principle, can provide the opportunity for a reproducible animal model system for degenerative joint diseases. However, previous attempts to engineer transgenic animals expressing MMPs such as MMP-1 and stromelysin have not resulted in an observable joint degeneration phenotype in the transgenic animals. This could be due to embryonic lethality caused by constitutive expression of these enzymes. Witty et al., *Mol.Biol. Cell* **6**:1287, 1995, have created transgenic animals that constitutively express MMP-1 and stromelysin in mammary tissue, but these animals do not exhibit symptoms of osteoarthritis. D'Armiento et al., *Cell* **71**:955, 1992, disclose transgenic mice that express human interstitial collagenase in the lung. Liu et al., *J. Cell Biol.* **130**:227, 1995, disclose transgenic animals that overexpress mutated type II collagen, resulting in

connective tissue defects but not osteoarthritis. None of these transgenic animal systems provides a useful animal model for osteoarthritis. Khokha et al., *Cancer and Metastasis Rev.* 14:97, 1995; Shapiro, *Matrix Biol.* 15:527, 1997.

Thus, there is a need in the art for animal model systems that mimic human degenerative joint diseases such as, e.g., osteoarthritis, rheumatoid arthritis, and chondrodysplasias. Transgenic animals containing regulatable heterologous genes whose expression results in cartilage degeneration are particularly advantageous in providing reproducible experimental control over the timing and the level of expression of the transgenes and, thereby, over the pathological syndrome itself. Such animals can be used to determine what level of expression of the transgene is required to cause disease and, importantly, can be used for drug discovery and optimization of treatment regimens. In particular, such transgenic animals can be used to further define the role of matrix-degrading enzymes in cartilage degradation and as an *in vivo* screen to identify compounds that modulate these enzymes or compounds that inhibit the progression of degenerative joint diseases.

Summary of the Invention

The present invention provides transgenic non-human animals or the progeny thereof whose somatic and germline cells contain, in stably integrated form, one or more heterologous or recombinant genes encoding polypeptides comprising enzymatically active matrix-degrading enzymes (MDEs), preferably MMPs. MMPs for use in the invention comprise one or more of MMP-1, MMP-2, MMP-3, MMP-7, MMP-8, MMP-9, MMP-10, MMP-11, MMP-12, MMP-13, MMP-14, MMP-15, MMP-16, and MMP-17; preferably one or more of MMP-1, MMP-3, MMP-8, and MMP-13; and most preferably one or more of

MMP-1 and MMP-13; and include enzymatically active variants, fragments, and combinations of these polypeptides. Other matrix-degrading enzymes can also be used, including, e.g., aggrecanase. The MDEs may be derived from any species, preferably human. In preferred embodiments, the recombinant MDE-encoding genes are selectively expressed in articular chondrocytes of the transgenic animal and expression results in pathological symptoms characteristic of degenerative joint disease.

In one aspect, the invention provides a transgenic animal or the progeny thereof whose somatic and germline cells contain a stably integrated first recombinant gene encoding an MDE or an enzymatically active derivative or variant thereof, preferably a constitutively active proMMP-13 variant (designated MMP-13*) comprising the sequence depicted in SEQ ID NO: 1. Preferably, the first recombinant gene is under the control of a first regulatable promoter; most preferably, the first regulatable promoter comprises a tetO7 sequence, such as, e.g., the promoter depicted in SEQ ID NO: 2. The transgenic animal may further comprise a second recombinant gene encoding a polypeptide that regulates the first regulatable promoter and is preferably a tTA polypeptide. In these embodiments, the second recombinant gene is under the control of a second regulatable promoter, preferably one that comprises sequences derived from a joint-specific promoter, and most preferably a type II collagen promoter, such as, e.g., the promoter depicted in SEQ ID NO: 3. Selective expression of the second recombinant gene in joint tissues thus results in regulated joint-specific expression of the recombinant MDE.

In another aspect, the invention provides isolated nucleic acids encoding enzymatically active MMP variants, preferably human proMMP-13 variants, and most preferably MMP-13*. The invention also encompasses recombinant cloning vectors

comprising these nucleic acids; cells comprising the vectors; methods for producing MMP-13-derived polypeptides comprising culturing the cells under conditions appropriate for MMP-13 expression; and isolated MMP-13-derived polypeptides.

In yet another aspect, the invention provides methods for producing phenotypic changes characteristic of cartilage-degenerative disease in a mammal, which comprise exposing the transgenic animals of the invention to conditions that result in expression of the MDEs encoded by the transgenes. In a preferred embodiment, a transgenic animal comprising a first recombinant gene encoding MMP-13* operably linked to a tetO7 promoter and a second recombinant gene encoding a tTA protein operably linked to a type II collagen promoter is maintained in the presence of tetracycline or a tetracycline analogue. When it is desired to induce expression of MMP-13*, tetracycline or the tetracycline analogue is withdrawn, MMP-13* is selectively expressed in joint tissues, and phenotypic changes characteristic of cartilage-degenerative disease result.

In yet another aspect, the invention provides methods for determining the potential of a composition to counteract cartilage-degenerative disease. The methods are carried out by administering a known dose of the composition to the transgenic animals of the invention, either before or after phenotypic indicators of cartilage-degenerative disease have developed; monitoring the indicators for a predetermined time following administration of the composition; and comparing the extent of the indicators in the animal to which the composition was administered relative to a control transgenic animal that had not been exposed to the composition. Any difference in (i) the nature or extent of phenotypic indicators of cartilage-degenerative disease, (ii) the time required for the indicators to

develop, or (iii) the need for other ameliorative treatments indicates the potential of the composition to counteract cartilage-degenerative disease.

5 **Brief Description of the Drawings**

Figure 1A is a schematic illustration of the structure of human MMP-13 (collagenase-3). The black box at the extreme aminotermminus represents the pre domain (signal peptide) that targets nascent proMMP-13 for secretion. The lightly hatched box represents the pro domain, which is involved in maintaining the latency of the enzyme. A conserved sequence within the pro domain that is important for maintaining enzyme latency is shown. The heavily hatched box represents the 170-amino acid catalytic domain, which contains a conserved region (shown) that is important for catalytic activity. The shaded box represents the 200-amino acid carboxyterminal domain.

Figure 1B is an illustration of the nucleic acid sequence encoding a constitutively active variant of human pro MMP-13, designated MMP-13*, and the amino acid sequence of MMP-13*, SEQ ID NO:1. The residues that are mutated relative to wild-type MMP-13, which are depicted in larger type, are GTC at nucleotide positions 299-301.

Figures 2A and 2B are schematic illustrations of transgenes used for regulated expression of human MMP-13* in transgenic mice. Figure 2A shows a nucleic acid construct comprising, in a 5' to 3' direction: (i) sequences derived from rat type II collagen promoter; (ii) sequences encoding a tetracycline repressor polypeptide fused in frame to sequences encoding a VP16 transcriptional activator polypeptide; and (iii) sequences comprising an SV40-derived RNA splice site and polyadenylation signal. Figure 2B shows a nucleic acid

construct comprising, in a 5' to 3' direction: (i) sequences derived from a bacterial tetO7 promoter; (ii) sequences encoding human MMP-13*; and (iii) sequences comprising an SV40-derived RNA splice site and polyadenylation signal.

Figure 3A is a schematic illustration of a transgene used to assess tissue-specific regulation conferred by a type II collagen promoter. The nucleic acid construct comprises, in a 5' to 3' direction: (i) sequences derived from a rat type II collagen promoter; (ii) sequences encoding bacterial β -galactosidase (LacZ); and (iii) sequences comprising an SV40-derived RNA splice site and polyadenylation signal.

Figure 3B is a color photographic illustration of whole mount staining for β -galactosidase activity of embryonic day 16 transgenic mouse embryos expressing the transgene illustrated in Figure 3A. Blue staining, indicating the presence of enzymatically active B-galactosidase polypeptides, is evident in joints throughout the body of the transgenic animal, while no staining is observed in the non-transgenic, wild-type littermate.

Figure 4 shows color photographic illustrations of immunohistochemical localization of type II collagen cleavage products in the growth plate and articular cartilage of transgenic mice expressing the transgenes shown in Figure 2. The tissues were stained with an antibody that recognizes cleavage products of type II collagen. The left panel shows tissue derived from a mouse that had been maintained on doxycycline to repress MMP-13* expression. The right panel shows tissue derived from a mouse that had been withdrawn from doxycycline, allowing expression of MMP-13*, for 30 days at 3 months of age.

Figure 5 is a color photographic illustration of Safranin O staining of the articular cartilage and growth plate of the patella of double transgenic mice. The left panel shows tissue derived from a mouse maintained on doxycycline. The middle panel shows

tissue derived from a mouse 7 days after withdrawal from doxycycline. The right panel shows tissue derived from a mouse 14 days after withdrawal from doxycycline.

Detailed Description of the Invention

5 The present inventors have discovered that regulated expression of matrix-degrading enzymes in cartilage in transgenic mice results in characteristic phenotypic changes associated with matrix degenerative diseases of the joints and intervertebral discs. The animal models of the invention provide novel model systems for matrix degenerative disease syndromes which can be used for detailed characterization of human joint and intervertebral
10 disc pathologies as well as for drug discovery and optimization of treatment regimens.

 A transgenic animal according to the invention is an animal having cells that contain a transgene which was introduced into the animal or an ancestor of the animal at a prenatal (embryonic) stage. A transgenic animal can be created, for example, by introducing the gene of interest into the male pronucleus of a fertilized oocyte by, e.g., microinjection,
15 and allowing the oocyte to develop in a pseudopregnant female foster animal. The gene of interest may include appropriate promoter sequences, as well as intronic sequences and polyadenylation signal sequences. Methods for producing transgenic animals are disclosed in, e.g., U.S. Patent Nos. 4,736,866 and 4,870,009 and Hogan et al., *A Laboratory Manual*, Cold Spring Harbor Laboratory, 1986. A transgenic founder animal can be used to breed
20 additional animals carrying the transgene. A transgenic animal carrying one transgene can also be bred to another transgenic animal carrying a second transgene to create a "double transgenic" animal carrying two transgenes. Alternatively, two transgenes can be co-microinjected to produce a double transgenic animal. Animals carrying more than two

transgenes are also possible. Furthermore, heterozygous transgenic animals, i.e., animals carrying one copy of a transgene, can be bred to a second animal heterozygous for the same transgene to produce homozygous animals carrying two copies of the transgene.

The present invention encompasses transgenic animals, preferably mammals, which express MDEs, particularly MMPs, and most particularly those MMPs having collagenase activity, from a recombinant gene. MDEs for use in the invention include without limitation MMPs and aggrecanase. Useful MMPs include without limitation the collagenases designated MMP-1, MMP-8 and MMP-13; the stromelysins designated MMP-3, MMP-10, and MMP-11; the gelatinases designated MMP-2 and MMP-9; the metalloelastase designated MMP-12; and membrane-type MMPs designated MMP-14, MMP-15, MMP-16, and MMP-17. Matrisian, *BioEssays*, 14:455, 1992. Matrix-degrading activity as used herein refers to the proteolytic degradation of matrix components, including, e.g., collagen, particularly type II collagen and most particularly the triple helical form of type II collagen. Any polypeptide exhibiting matrix-degrading activity may be used in practicing the invention, including enzymatically active fragments of the above-described enzymes. Preferably, MMP-13 enzymatic activity is expressed. MMP-13 enzymatic activity as used herein refers to the proteolytic degradation of type II collagen. Any MMP-13 polypeptide or fragment or derivative thereof that exhibits MMP-13 enzymatic activity may be used. The enzymes may be derived from any animal species, including without limitation human, mouse, rat, rabbit, pig, cow, or non-human primate, or combinations thereof. Preferably, the MMP-13 or derivative thereof is of human origin.

Normally, MMPs are synthesized as precursors (i.e., zymogens or proenzymes) whose enzymatic activity is latent; proteolytic removal of the pro region after secretion

produces the enzymatically active protein. In preferred embodiments of the invention, the need for proteolytic processing is circumvented by the use of enzyme or proenzyme variants that are enzymatically active even when uncleaved. Such variants can be produced using conventional techniques for site-directed or random mutagenesis coupled with analysis of collagenase enzymatic activity (see below). In this manner, modifications (including, e.g., insertions, deletions, and substitutions), may be introduced into a proenzyme sequence, particularly within the pro region or near the pro region cleavage site, to produce a constitutively active polypeptide which does not require proteolytic processing for activation. Alternatively, the pro region may be deleted entirely. Furthermore, recombinant genes may be used in which the sequence encoding the native signal peptide is replaced by a heterologous sequence that functions as a signal peptide, i.e., promotes secretion. The use of genes encoding any such modified MMP polypeptides is encompassed by the invention.

Preferably, a constitutively active MMP-13 variant is used in practicing the invention. Most preferably, the MMP-13 variant comprises a sequence containing a mutation in the sequence encoding the PRCGVPDV region, SEQ ID NO:4, specifically a substitution of Pro⁹⁹ to Val; the sequence of this polypeptide is depicted in SEQ ID NO: 1 and this polypeptide is designated MMP-13*. In another embodiment, the constitutively active MMP-13 variant comprises a substitution of Val⁹⁸ to Gly.

The transgenic animals of the invention preferably express MMP activity in a regulated manner. Regulated expression as used herein refers to temporal and/or spatial control. Temporal control refers to the ability to repress expression of MMP activity until a predetermined time in the development of the transgenic animal, after which MMP expression may be activated and maintained for as long as desired. Preferably, MMP

expression is repressed throughout embryonic development and activated in the adult animal. Spatial control refers to the ability to selectively express MMP activity in particular tissues. Preferably, MMP activity is selectively expressed in joint tissues, most preferably in articular chondrocytes.

5 Temporal control of MMP expression is achieved by use of one or more polypeptides comprising a transcriptional repressor, a transcriptional activator or enhancer, or combinations thereof, in conjunction with a promoter responsive to the transcriptional repressor/activator used to which the MMP-encoding sequence is operably linked. In one set of embodiments, temporal control of MMP expression is achieved by (i) expression in the
10 transgenic animal of a repressor polypeptide operably linked to a polypeptide that directly or indirectly activates transcription in eucaryotic cells, creating a repressor-activator fusion polypeptide; and (ii) the coupled use of a target promoter operably linked to an MMP-encoding sequence whose transcriptional activity is responsive to the repressor-activator fusion polypeptide. Typically, nucleotide sequences encoding the repressor polypeptide are
15 ligated in-frame to sequences encoding the transcriptional activator polypeptide to create a chimeric gene encoding a fusion protein.

Useful repressor polypeptides include without limitation polypeptides comprising sequences derived from bacterial repressors, including without limitation tetracycline repressor, LacR repressor, KRAB domain, and lambda repressor (cro and cI),
20 as well as eukaryotic repressors, including without limitation those involved in amino acid or sugar synthesis. Useful direct transcriptional activator polypeptides include without limitation herpes simplex virus protein 16 (VP16); yeast GAL14; yeast STAT; steroid receptors such as, e.g., progesterone receptor and estrogen receptor; and constitutive

activators such as, e.g., c-fos, c-jun, and SP-1. Alternatively, the repressor polypeptide may be linked to a polypeptide that indirectly activates transcription by recruiting a transcriptional activator to interact with the repressor-activator fusion protein; such indirect activator polypeptides include without limitation TATA Box Binding Protein (TBP) and basic transcription factors, including, e.g., basic transcription factor D.

According to the invention, each repressor-activator fusion protein is used in conjunction with a target promoter that is responsive to the particular fusion protein and that regulates transcription of an MDE-encoding sequence. Typically, the promoter comprises at least one operator sequence responsive to the repressor component of the repressor-activator fusion polypeptide, which is operably linked to at least a minimal promoter that supports transcription in eucaryotic cells. Examples of suitable repressor-responsive operator sequences include without limitation sequences derived from the tetracycline resistance operon encoded in Tn10 in *E. coli*, the lambda repressor operon, and the yeast GAL repressor operon. Examples of suitable eucaryotic promoters from which minimal promoters may be derived include without limitation the cytomegalovirus (CMV) IE promoter, PtK-1 (thymidine kinase) promoter, HSP (heat shock protein) promoter, and any eukaryotic promoter containing a TATA box. Minimal promoter sequences may be derived from these promoters by (i) creating deletion mutants using conventional methods and (ii) testing the ability of the resulting sequences to activate transcription in a cell line. U.S. Patent No. 5,650,298 discloses a repressor-activator fusion protein comprised of sequences derived from the tetracycline repressor fused to VP16 sequences, which is designated tTA, and a tTA-responsive promoter, designated tet07, which comprises a Tn10-derived sequence linked to a portion of the CMV IE promoter.

Alternatively, temporal control is achieved by (i) expression in the transgenic animal of a heterologous or recombinant transcriptional activator polypeptide or polypeptides and (ii) the coupled use of a target promoter operably linked to an MMP-encoding sequence whose transcriptional activity is responsive to the heterologous or recombinant transcriptional

5 activator. Useful transcriptional activators include without limitation a modified ecdysone receptor, in which a VP16 transactivation domain linked to the aminoterminal transactivation domain of the glucocorticoid receptor is fused to the ligand-binding domain and carboxyterminal sequence of the ecdysone receptor (No et al., *Proc. Natl. Acad. Sci. USA* 93:3346, 1996); a chimeric protein, designated pGL-VP, comprising VP16 activator

10 sequences, GAL4 activation sequences, and a mutated human progesterone receptor ligand-binding domain (Wang et al., *Proc. Natl. Acad. Sci. USA* 91:8180, 1994; Wang et al., *Gene Therapy* 4:432, 1997); and chimeric proteins comprising transcriptional activators fused to estrogen (or other steroid) binding domains (Mattioni et al., *Meth. Cell Biol.* 43:335, 1994).

The ecdysone receptor system utilizes retinoid X receptor (RXR) to form heterodimers with

15 the chimeric receptor, and responds to ecdysone, muristerone (an ecdysone analogue) or dexamethasone. The pGL-VP system is responsive to mifepristone (RU486). Chimeric receptors containing an estrogen binding domain respond to hydroxytamoxifen (an estrogen analogue).

Spatial control of MDE expression is achieved by the use of transcriptional

20 promoters that direct transcription selectively in joint tissues. Joint-specific expression as used herein refers to expression that is greater in joints than in other cells; typically, the level of expression in non-joint tissues is less than 10% of the level of expression in joints. Preferably, expression in non-joint tissues is undetectable. Useful promoter sequences that

confer joint-specific expression on a sequence to which they are operably linked include without limitation sequences derived from the collagen type II promoter. It will be understood that a joint-specific promoter according to the invention may comprise one or more copies of particular sequences or sub-sequences, and these sequences may be in direct or inverted orientation relative to each other and relative to the sequence whose expression is regulated by the promoter.

Coordinated spatial and temporal control of MDE expression is preferably achieved by (i) placing expression of the repressor-activator fusion polypeptide or the transcriptional activator polypeptide under the control of a joint-specific promoter; (ii) placing the expression of the MDE or a derivative thereof under the control of a promoter responsive to the repressor-activator fusion polypeptide or the transcriptional activator polypeptide; and (iii) maintaining the transgenic animal during fetal development and early life under conditions in which MDE expression is repressed.

The method by which transgenic animals are maintained during fetal and early post-natal development so that MDE expression is repressed will depend on the particular transgenes being expressed. When a repressor-activator fusion polypeptide is used, repression is achieved by providing the animal with an agent that binds to the repressor-activator fusion protein and results in repression of transcription of the target MDE gene. In animals comprising a transgene encoding a repressor-activator fusion polypeptide containing tet repressor sequences, repression is achieved by providing tetracycline or a tetracycline analogue in the food or drinking water of the mother and, following birth, of the progeny. Tetracycline or an analogue may also be provided using surgically implanted subcutaneous time-release pellets (Innovative Research of America, Inc., Sarasota FL) In this case, binding

of tetracycline or a tetracycline analogue to the repressor-activator fusion protein prevents the fusion protein from binding to, and activating transcription of, the cognate promoter. Tetracycline analogues are compounds closely related to tetracycline which bind to the tet repressor with a K_a of at least about $10^6 M^{-1}$, preferably with an affinity of about $10^9 M^{-1}$ or greater. Useful tetracycline analogues include without limitation doxycycline, anhydrotetracycline, chlortetracycline, epioxytetracycline, and the like. The dosage used is one that will result in substantial repression of MMP expression. Typically, tetracycline or a tetracycline analogue is administered in the animal's drinking water at a dosage of about 1 mg/ml. When it is desired that MMPs be expressed, the tetracycline or analogue thereof is withheld.

In other embodiments, repression is achieved by withholding from the animal an agent required for activity of the transcriptional activator polypeptide. For example, if the transcriptional activator is a modified ecdysone receptor, the animals are maintained in the absence of ecdysone or an ecdysone analogue throughout fetal and early post-natal development. Ecdysone analogues are compounds closely related to ecdysone which bind to the modified ecdysone receptor with a K_a of at least about $10^6 M^{-1}$. Useful ecdysone analogues include without limitation muristerone A. When it is desired that MDEs be expressed, the animals are given, e.g., ecdysone or muristerone A via intraperitoneal injections at dosages of between about 10 mg and about 20 mg/animal. Similarly, when pGL-VP is used, activation is achieved by providing mifepristone.

In a preferred embodiment of the invention, a transgenic animal is constructed whose somatic and germline cells contain in stably integrated form two recombinant genes: (i) a first recombinant gene comprising a sequence encoding MMP-13*, wherein the sequence

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is operably linked to a tetO7 promoter; and (ii) a second recombinant gene encoding a tTA protein operatively linked to a collagen type II promoter. In this embodiment, animals are maintained in the presence of tetracycline or a tetracycline analogue throughout fetal and early post-natal development to repress the gene. Afterwards, tetracycline or the tetracycline analogue is withdrawn, and MMP-13 enzymatic activity is selectively expressed in joint tissues.

Animal Models for Cartilage-Degenerative Diseases

The present invention provides animal model systems in which phenotypic changes characteristic of cartilage-degenerative diseases, such as, e.g., joint or disc disease, are reproducibly exhibited. These diseases include without limitation osteoarthritis, rheumatoid arthritis, chondrodysplasias, and degenerative intervertebral disc diseases. The model systems of the invention exhibit one or more phenotypic indicators common to these diseases, which include without limitation loss of proteoglycan (as indicated by, e.g., loss of Safranin O staining) and cleavage of type II collagen in the affected tissues. The systems encompass the transgenic animals described above, in which recombinant or heterologous MDEs, particularly MMPs, are expressed in cartilage at a predetermined time in the life of the transgenic animal. The timing of the appearance of cartilage-degenerative indicators is determined by activating MDE expression and monitoring the effects on cartilage (see below). Preferably, one or more MDEs are expressed after birth, most preferably after the animal has reached adulthood.

Expression of the transgenes is typically monitored by extracting mRNA from different tissues and subjecting the extracted mRNA to one or more of the following: (i)

reverse transcriptase-polymerase chain reaction (RT-PCR), using primers homologous to the transgene; (ii) RNAase protection; and (iii) Northern blot analysis. Alternatively, in situ hybridization may used.

The physiological effects of MDE expression on articular cartilage are monitored in test animals by sacrificing the animals and subjecting paraffin-embedded decalcified cartilage to staining with (i) hematoxylin and eosin (using conventional techniques) followed by double staining with (ii) Safranin O and fast green. Peter et al., *J. Exp. Pathol.* 71:19, 1990. Alternatively, frozen sections may be obtained and stained with antibodies that are specific for cleavage fragments derived from type II collagen. Billingham et al., *J. Clin. Invest.* 99:1534, 1997. Typically, expression of the MMP transgene(s) for at least about 7 days results in detectable loss of proteoglycan and changes in growth plate morphology (see, e.g., Example 5 below). Animal models in which expression of MDEs, particularly MMPs, and most particularly an enzymatically active form of MMP-13, results in proteoglycan loss and/or cleavage of type II collagen are within the scope of the invention.

Other phenotypic indicators of cartilage-degenerative disease which can be monitored in transgenic animals produced according to the invention include without limitation gross observations of changes in joint function and histological evidence of (i) fibrillation and loss of articular cartilage and (ii) osteophyte formation.

Syndromes for which the transgenic animals of the invention provide useful models include without limitation any pathological condition that manifests a disturbance in the composition, morphology, and/or function of cartilage, including osteoarthritis; rheumatoid arthritis; degenerative intervertebral disc diseases; chondrodysplasias, including, e.g., Kniest dysplasia, achondrogenesis, and hypophosphatasia; and proteoglycan-mediated

disorders, such as occur, e.g., in brachymorphic animals. Hall et al., *Cartilage: Molecular Aspects*, CRC Press, 1991, pp. 201-203.

In further embodiments of the invention, the transgenic animals can be subjected to additional treatments to modulate the cartilage-degenerative indicators and/or to supplement the animals' disease phenotype with additional physiological effects such as, e.g., those associated with a particular disease. For example, the transgenic animals may be further treated with inflammatory mediators to augment collagen degradation and/or induce loss of proteoglycan (see, e.g., Example 6 below). Furthermore, the timing and extent of MDE induction, with or without additional treatments, can be adapted to replicate the symptomatology of a particular disease or syndrome.

Methods for Evaluating Drugs that Modulate Degenerative Diseases of Cartilage

The present invention encompasses methods for discovery and evaluation of drugs and therapies for their efficacy against degenerative diseases of cartilage, particularly degenerative joint diseases. In one embodiment of the invention, the transgenic animals of the invention are maintained under conditions in which expression of one or more MDEs results in one or more phenotypic indicators of cartilage-degenerative disease. Once the symptoms have developed, the potential of a composition to counteract cartilage-degenerative disease can be evaluated by administering a known dose of the composition to the animal in which the symptoms have developed; monitoring the phenotypic indicators for a predetermined time following administration of the composition; and comparing the extent of the phenotypic indicators in the animal to which the composition was administered relative to a control animal. Control animals comprise age- and sex-matched transgenic animals that

are maintained under an identical regimen (i.e., express the transgenes) but which do not receive the composition. Any statistically significant difference in the extent or nature of the phenotypic indicators indicates the potential of the composition to counteract cartilage-degenerative disease. As used herein, phenotypic indicators of cartilage-degenerative disease
5 refer to proteoglycan loss, joint space narrowing, collagen degradation, and destruction of cartilage.

In another embodiment of the invention, the potential of a composition to counteract degenerative diseases of cartilage, particularly degenerative joint disease, is evaluated by administering to a transgenic animal a known dose of the composition before
10 and/or simultaneous with the induction of MDE expression in the transgenic animal; monitoring phenotypic indicators of cartilage-degenerative disease for a predetermined time following administration of the composition and MDE induction; and comparing the extent of the phenotypic indicators and/or disease in the animal to which the composition was administered relative to a control animal that had not been exposed to the composition. In
15 this embodiment, any statistically significant difference in the extent or nature of the phenotypic indicators and/or disease, or any statistically significant delay in appearance of the phenotypic indicators or disease, indicates the potential of the composition to counteract cartilage-degenerative disease.

A further indication of the potential of a composition to counteract cartilage-
20 degenerative disease is the ability of the composition to cause any reduction in the extent or duration of other treatments, including, e.g., the dosage and timing of administration of other therapeutic agents used to alleviate symptoms of the disease.

Compounds that may be tested for anti-cartilage-degenerative disease potential may be found in, for example, natural product libraries, fermentation libraries (encompassing plants and microorganisms), combinatorial libraries, compound files, synthetic compound libraries, and compounds resulting from directed rational drug design and synthesis. For example, synthetic compound libraries are commercially available from Maybridge Chemical Co. (Trevillet, Cornwall, UK), Comgenex (Princeton, NJ), Brandon Associates (Merrimack, NH), and Microsource (New Milford, CT). A rare chemical library is available from Aldrich Chemical Company, Inc. (Milwaukee, WI). Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available from, for example, Pan Laboratories (Bothell, WA) or MycoSearch (NC), or are readily producible. Additionally, natural and synthetically produced libraries and compounds are readily modified through conventional chemical, physical, and biochemical means. Blondelle et al., *TibTech* 14:60, 1996.

Transgenic animals

Transgenic animals as used herein refers to animals into which one or more heterologous and/or recombinant genes have been introduced. The transgenes may be from a different species, or from the same species as the transgenic animal but are not naturally found in the animal in the configuration and/or at the chromosomal locus conferred by the transgene. Transgenes may comprise foreign DNA sequences, i.e., sequences not normally found in the genome of the host animal. Alternatively or additionally, transgenes may comprise endogenous DNA sequences that have been rearranged or mutated *in vitro* in order to alter the normal *in vivo* pattern of expression of the gene, or to alter or eliminate the

biological activity of an endogenous gene product encoded by the gene. Also encompassed by the invention are DNA fragments that are introduced into a pre-existing gene to, e.g., change patterns of expression or to provide additional means of regulating the expression of the gene. Watson et al., "The Introduction of Foreign Genes Into Mice," in *Recombinant*
 5 *DNA*, 2d Ed., W.H. Freeman & Co., New York, 1992, pp. 255-272; Gordon, J.W., *Intl. Rev. Cytol.* 115:171, 1989; Jaenisch, *Science* 240:1468, 1989; Rossant, *Neuron* 2:323, 1990.

The transgenic non-human animals of the invention are produced by introducing transgenes into the germline of the non-human animal. Embryonal target cells at various developmental stages are used to introduce the transgenes of the invention.
 10 Different methods are used depending on the stage of development of the embryonal target cell(s). Such methods include, but are not limited to, microinjection of zygotes, viral integration, and transformation of embryonic stem cells as described below.

1. Microinjection of zygotes is the preferred method for incorporating transgenes into animal genomes. A zygote, which is a fertilized ovum that has not undergone
 15 pronuclei fusion or subsequent cell division, is the preferred target cell for microinjection of transgenic DNA sequences. The murine male pronucleus reaches a size of approximately 20 micrometers in diameter, a feature which allows for the reproducible injection of 1-2 picoliters of a solution containing transgenic DNA sequences. The use of a zygote for introduction of transgenes has the advantage that, in most cases, the injected transgenic DNA
 20 sequences will be incorporated into the host animal's genome before the first cell division. Brinster et al., *Proc. Natl. Acad. Sci. USA* 82:4438, 1985. As a consequence, all cells of the resultant transgenic animals (founder animals) stably carry an incorporated transgene at a particular genetic locus, referred to as a transgenic allele. The transgenic allele

demonstrates Mendelian inheritance, i.e., half of the offspring resulting from the cross of a transgenic animal with a non-transgenic animal will inherit the transgenic allele, in accordance with Mendel's rules of random assortment.

2. Viral integration can also be used to introduce the transgenes of
5 the invention into an animal. The developing embryos are cultured *in vitro* to the blastocyte developmental stage. The blastomeres may be infected with appropriate retroviruses. Jaenich, *Proc. Natl. Acad. Sci. USA* **73**:1260. Infection of the blastomeres is enhanced by enzymatic removal of the zona pellucida. Transgenes are introduced via viral vectors which are typically replication-defective but which remain competent for integration of viral-associated
10 DNA sequences, including transgenic DNA sequences linked to such viral sequences, into the host animal's genome. Transfection is easily and efficiently obtained by culture of blastomeres on a monolayer of cells producing the transgene-containing viral vector. Alternatively, infection may be performed using cells at a later developmental stage, such as blastocoeles. In any event, most transgenic founder animals produced by viral integration
15 will be mosaics for the transgenic allele; that is, the transgene is incorporated into only a subset of all the cells that form the transgenic founder animals. Moreover, multiple viral integration events may occur in a single founder animal, generating multiple transgenic alleles which will segregate in future generations of offspring. Introduction of transgenes into germline cells by this method is possible but probably occurs at a low frequency. However,
20 once a transgene has been introduced into germline cells by this method, offspring may be produced in which the transgenic allele is present in all of the animal's cells, i.e., in both somatic and germline cells.

3. Embryonal stem (ES) cells can also serve as target cells for introduction of the transgenes of the invention into animals. ES cells are obtained from pre-implantation embryos that are cultured in vitro. Evans et al., *Nature* 292:154, 1981. ES cells that have been transformed with a transgene can be combined with an animal blastocyst, after which the ES cells colonize the embryo and contribute to the germline of the resulting animal (which is a chimera, i.e., composed of cells derived from two or more animals). Again, once a transgene has been introduced into germline cells by this method, offspring may be produced in which the transgenic allele is present in all of the animal's cells, i.e., in both somatic and germline cells.

Although the initial introduction of a transgene is a Lamarckian (non-Mendelian) event, the transgenes of the invention may be stably integrated into germ line cells and transmitted to offspring of the transgenic animal as Mendelian loci. Other transgenic techniques result in mosaic transgenic animals, in which some cells carry the transgenes and other cells do not. In mosaic transgenic animals in which germ line cells do not carry the transgenes, transmission of the transgenes to offspring does not occur. Nevertheless, mosaic transgenic animals are capable of demonstrating phenotypes associated with the transgenes.

In practicing the invention, animals of the transgenic maintenance line are crossed with animals having a genetic background in which expression of the transgene results in symptoms of cartilage-degenerative disease. Offspring that have inherited the transgenes of the invention are distinguished from littermates that have not inherited transgenes by analysis of genetic material from the offspring for the presence of nucleic acid sequences derived from the transgenes of the invention. For example, biological fluids that contain polypeptides uniquely encoded by the transgenes of the invention may be immunoassayed for the presence

of the polypeptides. A simpler and more reliable means of identifying transgenic offspring comprises obtaining a tissue sample from an extremity of an animal, such as, for example, a tail, and analyzing the sample for the presence of nucleic acid sequences corresponding to the DNA sequence of a unique portion or portions of the transgenes of the invention. The presence of such nucleic acid sequences may be determined by, e.g., hybridization ("Southern") analysis with DNA sequences corresponding to unique portions of the transgene, analysis of the products of PCR reactions using DNA sequences in a sample as substrates, oligonucleotides derived from the transgene's DNA sequence, and the like.

10 Nucleic Acids, Vectors, Expression Systems, and Polypeptides

The present invention encompasses isolated nucleic acids encoding MDEs, particularly MMPs, and enzymatically active fragments derived therefrom, as well as constitutively active MMP variants and enzymatically active fragments derived therefrom. The invention also encompasses complements of the above nucleic acids; vectors comprising the nucleic acids; cells comprising the vectors; and isolated polypeptides encoded by the nucleic acids.

Many techniques in molecular biology, microbiology, recombinant DNA, and protein biochemistry are used in practicing the present invention, such as those explained in, for example, Sambrook *et al.*, 1989, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York; *DNA Cloning: A Practical Approach*, Volumes I and II, 1985 (D.N. Glover ed.); *Oligonucleotide Synthesis*, 1984, (M.L. Gait ed.); *Transcription and Translation*, 1984 (Hames and Higgins eds.); *A Practical Guide to Molecular Cloning*; the series, *Methods in Enzymology* (Academic

Press, Inc.); and *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.).

"Nucleic acid" or "polynucleotide" as used herein refers to purine- and pyrimidine-containing polymers of any length, either polyribonucleotides or polydeoxyribonucleotides or mixed polyribo-polydeoxyribo nucleotides. This includes single- and double-stranded molecules, such as, for example, DNA-DNA, DNA-RNA and RNA-RNA hybrids, as well as "protein nucleic acids" (PNA) formed by conjugating bases to an amino acid backbone. This also includes nucleic acids containing modified bases.

A "coding sequence" or a "protein-coding sequence" is a polynucleotide sequence capable of being transcribed into mRNA and/or capable of being translated into a polypeptide. The boundaries of the coding sequence are typically determined by a translation start codon at the 5'-terminus and a translation stop codon at the 3'-terminus.

A "complement" of a nucleic acid sequence as used herein refers to the "antisense" sequence that participates in Watson-Crick base-pairing with the original sequence.

An "isolated" nucleic acid or polypeptide as used herein refers to a component that is removed from its original environment (for example, its natural environment if it is naturally occurring). An isolated nucleic acid or polypeptide typically contains less than about 50%, preferably less than about 75%, and most preferably less than about 90%, of the cellular components with which it was originally associated.

A nucleic acid or polypeptide sequence that is "derived from" a designated sequence refers to a sequence that corresponds to a region of the designated sequence. For nucleic acid sequences, this encompasses sequences that are homologous or complementary

Sequence-conservative variants are those in which a change of one or more nucleotides in a given codon position results in no alteration in the amino acid encoded at that position.

10 to elicit antibodies specific to a designated polypeptide.

15 or other well known methods. This can be performed by sequentially linking a series of
oligonucleotide cassettes comprising pairs of synthetic oligonucleotides.

20 systems. Such degenerate variants are also encompassed by this invention.

The nucleic acids may also be modified by many means known in the art. Non-limiting examples of such modifications include methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such

as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoroamidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.). Nucleic acids may contain one or more additional covalently linked moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), intercalators (e.g., acridine, psoralen, etc.), chelators (e.g., metals, radioactive metals, iron, oxidative metals, etc.), and alkylators. PNAs are also encompassed by the term "nucleic acid". The nucleic acid may be derivatized by formation of a methyl or ethyl phosphotriester or an alkyl phosphoramidate linkage. Furthermore, the nucleic acid sequences of the present invention may also be modified with a label capable of providing a detectable signal, either directly or indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and the like.

The polypeptides of the invention may be expressed by using many known vectors, such as pUC plasmids, pET plasmids (Novagen, Inc., Madison, WI), or pRSET or pREP plasmids (Invitrogen, San Diego, CA), and many appropriate host cells, using methods disclosed or cited herein or otherwise known to those skilled in the relevant art. The particular choice of vector/host is not critical to the practice of the invention. Recombinant cloning vectors will often include one or more replication systems for cloning or expression; one or more markers for selection in the host, such as, for example, antibiotic resistance; and one or more expression cassettes. The inserted coding sequences may be synthesized by standard methods, isolated from natural sources, prepared as hybrids, or the like. Ligation of the coding sequences to transcriptional regulatory elements and/or to other amino acid coding sequences may be achieved by known methods. Suitable host cells may be transformed/transfected/infected as appropriate by any suitable method including

electroporation, CaCl_2 mediated DNA uptake, fungal infection, microinjection, microprojectile, or other established methods.

Appropriate host cells include bacteria, archebacteria, fungi, yeast, plant, and animal cells, and especially mammalian cells. Of particular interest are *E. coli*, *S. aureus*,
5 *B. subtilis*, *Saccharomyces cerevisiae*, *Saccharomyces carlsbergensis*, *Schizosaccharomyces pombe*, SF9 cells, C129 cells, 293 cells, *Neurospora*, CHO cells, COS cells, HeLa cells, and immortalized mammalian myeloid and lymphoid cell lines. Preferred replication systems include M13, ColE1, SV40, baculovirus, lambda, adenovirus, cytomegalovirus, and the like. A large number of transcription initiation and termination regulatory regions have been
10 isolated and are effective in the transcription and translation of heterologous proteins in the various hosts. Examples of these regions, methods of isolation, manner of manipulation, etc. are known in the art (Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley, 1997). Under appropriate expression conditions, host cells can be used as a source of recombinantly produced peptides and polypeptides.

15 The MDEs of the present invention, including function-conservative variants, may be isolated from native or heterologous organisms or cells (including, but not limited to, bacteria, fungi, insect, plant, and mammalian cells) into which the protein-coding sequence has been introduced and expressed. Alternatively, these polypeptides may be produced in cell-free protein synthesis systems, which may additionally be supplemented with microsomal
20 membranes to achieve glycosylation and signal peptide processing of procollagenases. Furthermore, the polypeptides may be chemically synthesized by commercially available automated procedures, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation, or classical solution synthesis.

Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. For some purposes, it is preferable to produce the polypeptide in a recombinant system in which the protein contains an additional sequence tag that facilitates purification, such as, but not limited to, a polyhistidine sequence. The polypeptide can then be purified from a crude lysate of the host cell by chromatography on an appropriate solid-phase matrix. Alternatively, antibodies produced against the protein or against peptides derived therefrom can be used as purification reagents. Other purification methods are possible.

The construction and analysis of MMP variants and derivatives that exhibit enzymatic activity, and preferably constitutive enzymatic activity, can be achieved by routine application of conventional methods. First, a nucleic acid encoding an MMP is modified either by site-directed or random mutagenesis, or is used in a construction scheme as one segment of a fusion gene. Preferably, the procedure results in a modification either contained within the sequence encoding the pro region or near the pro region cleavage site; this includes deleting the pro region entirely. Alternatively, sequences may be constructed that encode fusion proteins either between enzymatically active MMP domains and other polypeptides, or between different MMPs. The modified nucleic acid is then used to program synthesis of a variant MMP, either in a cell-free system, in intact cells (including permeabilized cells), or in a transgenic animal. Preferably, either a cell-free system or a cell culture system is used to express the MMP variant or derivative. The extent of pro region cleavage is assessed by metabolic labelling and resolution of the MMP product by SDS-PAGE. Finally, MMP enzymatic activity is measured using conventional assays, such as, by quantifying the

5 routinely and assayed for MMP enzymatic activity.

Description of the Preferred Embodiments

The following examples are intended to illustrate the present invention without limitation.

5 Example 1: Construction of a Gene Encoding a Modified, Constitutively Active ProMMP-13

The following experiments were performed to create a gene encoding a procollagenase derived from MMP-13 that is enzymatically active in the absence of pro region cleavage. The sequence of this proMMP-13 variant, designated MMP13*, is shown
10 in Figure 1B, SEQ ID NO:1.

Site-directed mutagenesis was performed to modify MMP-13 cDNA as follows:

A cDNA fragment encoding proMMP was obtained by digesting plasmid pNot3A (Freije et al., *J. Biol. Chem.* **269**:16766, 1994; GENBANK accession number X75308) with XbaI and HindIII and purifying the resulting ~1515 bp fragment. This fragment was
15 subcloned into the Tet-resistant/Amp-sensitive pAlter plasmid (Promega, Madison, WI) that had been digested with XbaI and HindIII.

Site-directed mutagenesis was performed using the Altered Sites II in vitro Mutagenesis System (Promega, Madison, WI). Briefly, phagemid single-stranded DNA was purified from cultures containing the helper phage R408 (Promega). In addition to the Amp
20 repair - Tet knock-out conversion oligos (Promega), an oligonucleotide having the sequence 5'-AAGCCAAGATGCGGGGTTGTCGATGTGGGTGAATACAAT-3', SEQ ID NO:5, was phosphorylated and annealed to the single-stranded DNA, followed by mutant strand synthesis. The reaction mixture was then used to transform the repair-minus *E. coli* strain

ES1301 *mutS*, and the culture was grown in ampicillin selective media. Plasmid DNA was isolated from isolated clones and transformed into JM109 cells, which were then plated on LB plates containing 120 µg/ml ampicillin.

The above procedure resulted in a proline-to-valine substitution at amino acid 99.

- 5 The modified proMMP was designated MMP13* (Figure 1B, SEQ ID NO:1).

Using a similar technique, site-directed mutagenesis was also used to introduce a valine to glycine mutation at amino acid 98. A mutagenic oligonucleotide having the sequence 5'-GAAAAAGCCAAGATGCGGGGGTCCTGATGTGGGTGAATAC-5', SEQ ID NO:6 was used as described above. This procedure resulted in a valine-to-glycine
10 substitution at amino acid 98.

After confirmation of the above mutations by direct sequencing, cDNA encoding MMP13* cDNA was excised from the pAlter vector by digestion with Eco RI and Hind III.

The enzymatic activity of MMP-13* was determined as follows:

- 15 1. cDNAs encoding both mutant forms of MMP13 and wild-type MMP-13 were subcloned into a BS(SK-) vector (Stratagene) containing the CMV promoter (Xho I - Eco RI) and the SV40 splice poly (A)n (Xba I - Nco I). Duplicate cultures of Hela cells (10 cm dishes) were transfected with 50 µg of these plasmids using the CaPO₄ precipitation method (Promega). Five hours later, cells were subjected to a 1-minute glycerol shock using a
20 solution containing an equal volume of 2 X HBS + 30 % glycerol. This procedure is described in the Profection Mammalian Transfection Systems technical manual (Promega).

2. Twenty-four hours following transfection, the culture medium (D-MEM containing 10 % fetal bovine serum) was replaced with D-MEM containing no serum and 10

μ M CGS-27023A (Ciba-Geigy), an MMP inhibitor. It is believed that, in the absence of an added MMP inhibitor, MMPs produced by the culture autodigest; thus, addition of an MMP inhibitor to the culture medium resulted in a detectable MMP13 band.

3. Forty-eight hours after the addition of serum-free medium containing the MMP inhibitor, 10 ml of supernatant were collected and concentrated about 200-fold using Centriprep-30 and Centricon-10 concentrators (Amicon), after which an equal volume of 2X Tris-glycine SDS running buffer was added to each sample. The samples were then applied to a 4-16% pre-stained beta-casein zymogram SDS polyacrylamide gel (Novex). After electrophoresis, the gels were renatured in renaturing buffer (Novex) for 30 minutes at room temperature, followed by overnight incubation at 37°C in zymogram developing buffer (Novex).

The results indicated that cells expressing either a variant MMP13 containing a proline -> valine substitution at position 99 (MMP-13*) or a variant MMP13 containing a valine -> glycine substitution at position 98 secreted detectable MMP activity similar to cells expressing wild-type MMP-13. This method thus provides a rapid screen for MMP13 variants that retain MMP13 enzymatic activity.

In a further step, cDNA encoding MMP-13* was operably linked to a transcriptional regulatory sequence derived from the tet07 promoter as follows:

1. The BS(SK-) vector (Stratagene) was digested with KpnI and NotI. A synthetic duplex oligonucleotide having the following sequence was digested with KpnI and Not I and ligated to the vector:

5'-GGTACCACTAGTAAGCTTAGATCTCATATGGTCGACCCCGGGGAATTCCTGCA
GGGATCCTCTAGAAGTACTCCATGGGTATACATCGATGCGGCCGC-3', SEQ ID
NO:7

The SB(SK-) vector as modified above was digested with XbaI and NcoI. A 745
5 bp fragment containing the SV40 splice site and polyadenylation signal, which was obtained
by digesting pcDNAI/Amp (Invitrogen, Carlsbad, CA) with XbaI and NcoI, was ligated to
this vector. This 745 bp fragment was recovered by digestion of the vector with XbaI and
NotI and was inserted into the original BS(SK-) vector.

2. The resulting vector was linearized by digestion with XhoI and EcoRI and
10 ligated to a 460 bp XhoI-EcoRI fragment containing the tetO7 promoter region (Gossen et al.,
Proc. Natl. Acad. Sci. USA **89**:5547, 1992). This vector was then digested with SpeI, blunt-
ended with Klenow polymerase, and digested with EcoRI.

3. pAlter-MMP13* was digested with HindIII, blunt-ended with Klenow
polymerase, and digested with EcoRI to obtain an MMP13*-encoding fragment.

15 4. The MMP13* EcoRI fragment was cloned into the EcoRI digested vector
obtained in step 2.

5. The 2792 bp transgene, SEQ ID NO:8, was excised by digestion with XhoI
and NotI and purified using CsCl gradient centrifugation.

20 Example 2: Construction of a Collagen Type II-Promoter-Linked tTa gene

The following experiments were performed to create a gene encoding a tTA
repressor-activator fusion protein operably linked to a joint-specific (type II collagen)

promoter as well as a reporter gene suitable for assessing the tissue-specific expression conferred by the type II collagen promoter.

1. *Type II collagen promoter-tetracycline/VP16 transgene*: The modified BS(SK-) vector containing the SV40 splice site and polyadenylation signal as described in Example 1 above was digested with NdeI and Sma I and ligated to a 1897 bp fragment containing the collagen II promoter and enhancer. This fragment was obtained by digesting plasmid PBS△H1 with HindIII, after which it was blunt-ended with Klenow and digested with NdeI.

The plasmid was then digested with EcoRI and BamHI and ligated to a 1025 bp fragment encoding the tetracycline/VP16 repressor-activator fusion protein that had been excised from the pUHG15-1 plasmid (Gossen et al., *Proc. Natl. Acad. Sci. USA* **89**:5547, 1992) using EcoRI and BamHI. The plasmid was linearized by digestion with BglII, dephosphorylated using calf intestinal phosphatase, and ligated to a 1554 BamHI enhancer fragment obtained from plasmid PBS△H1.

Finally, the 5276 bp transgene, SEQ ID NO:9, was excised from the vector by digestion with KpnI and NotI, gel purified, purified by CsCl gradient centrifugation, dialyzed against microinjection buffer (5 mM Tris-HCl pH 7.4, 0.1 mM EDTA pH 8.0) and used for microinjection (see Example 3 below).

2. *Type II collagen promoter-β-galactosidase gene*: A 4179 bp BamHI-BglII fragment containing the β-galactosidase gene fused to the β-globin splice sequence and polyadenylation signal was excised from plasmid pUGH16-3 (Gossen et al., *Proc. Natl. Acad. Sci. USA* **89**:5547, 1992) and cloned into the BamHI site of unmodified BS(SK-) (Stratagene). This plasmid was digested with EcoRI and HindIII and ligated to a 655 bp Hind III-Eco RI

fragment containing the type II collagen promoter sequence, which was excised from the plasmid described in (1) above. The plasmid was then digested with EcoRI and ligated to a 2807 bp Eco RI fragment which had been excised from the type II collagen promoter plasmid described above. Restriction mapping was used to verify the orientation of each insert. The 7664 bp transgene, SEQ ID NO:10, was excised by digestion with HindIII and NotI, gel purified, purified by CsCl gradient centrifugation, dialyzed against microinjection buffer (5 mM Tris pH 7.4, 0.1 mM EDTA pH 8.0), and microinjected into mouse embryos.

Example 3: Production and Characterization of Transgenic Mice Expressing Tetracycline-Regulated MMP-13 in Joint Tissues

The following experiments were performed to produce transgenic mice expressing MMP-13* or a LacZ (β -galactosidase) reporter gene.

To produce mice expressing MMP-13* under tetracycline regulation, an XhoI-NotI tet07-MMP-13* DNA fragment (Figure 2B, SEQ ID NO:8) and a KpnI - NotI CPE-tTA DNA fragment (Figure 2A, SEQ ID NO:9) were co-microinjected into fertilized mouse embryos in equimolar amounts. To produce mice expressing the reporter gene, a HindIII-NotI LacZ fragment (described in Example 2 above) was injected into (FVB/N) fertilized eggs as described (Hogan et al., *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratories, 1996).

Founder animals were first identified by PCR as follows. The tTA-encoding transgene was identified using a primer corresponding to the tTA sequence (5'-CGAGGGCCTGCTCGATCTCC-3', SEQ ID NO:11) and a primer corresponding to a 3' untranslated sequence (5'-GGCATTCCACCACTGCTCCC-3', SEQ ID NO:12). The

resulting PCR product was 584 bp in size. The MMP13* -encoding transgene was identified using primers corresponding to sequences encoding MMP13* (5'-GAGCACCTTCTCATGACCTC-3', SEQ ID NO:13) and the 3' untranslated region, respectively. The resulting PCR product was 731 bp in size. Out of 112 newborn mice, 7 transgenic founders harboring both transgenes were found.

The LacZ-encoding transgene was identified using primers corresponding to the nuclear localization signal of the β -galactosidase gene (5'-GTTGGTGTAGATGGGCGCATCG-3', SEQ ID NO:14) and the collagen promoter (5'-GCGGGGTCTCAGGTTACAGCC-3', SEQ ID NO:15). The resulting PCR product was 673 bp in size.

Southern blot analysis of tail DNA digested with BamHI/NcoI or PvuII/NcoI and hybridized to the 3' untranslated region under high stringency conditions was performed to confirm the results obtained using PCR. The number of copies of transgene DNA that integrated into the genome was determined by comparing the relative intensity of the hybridization signal from transgenic mice with that obtained using control DNAs containing 10 and 100 genome equivalents of the same DNA that was injected. Transgenic lines were generated by mating founder animals to FVB/N wild type animals.

All mice were administered doxycycline (Sigma Chemical Co., St. Louis MO) at a concentration of 1.0 mg/ml in acidic drinking water, which was changed on a daily basis.

Schultze et al., *Nature Biotech.* **14**:499, 1996.

Example 4: Analysis of Joint-Specific Expression Conferred by Type II Collagen Promoter Constructs

The following experiments were performed to evaluate tissue-specific expression conferred by use of the type II collagen promoter.

5 Joint-specific expression was monitored by staining for β -galactosidase activity as described (Hogan et al., *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratories, 1996); using this method, the presence of enzymatically active β -galactosidase is reflected in the appearance of a blue stain.

10 Wild-type female mice were mated with transgenic males harboring the CPE-LacZ construct as described in Examples 2 and 3 above. On embryonic day 16, the females were sacrificed, and the embryos were stained for β -galactosidase activity. Prior to fixation, the tails were removed from the embryos and used as a source of template DNA for PCR reactions to determine transgene transmission.

15 Figure 3B illustrates the blue staining that is observed in joints throughout the body of the embryonic day 16 transgenic mouse embryo. Specifically, β -galactosidase expression was observed in ankles, knees, hips, phalanges, wrists, elbows, shoulders, and vertebrae. In addition to the cartilage of the joints, cartilage that had not ossified to bone at this stage of development, *i.e.*, some of the facial, skull, and rib bones, also expressed β -galactosidase. No staining was observed in non-transgenic, wild type littermates.

20 These results indicated that the type II collagen-derived promoter according to the present invention is capable of conferring joint-specific expression on sequences to which it is operably linked.

The following experiments were performed to evaluate the development of phenotypic indicators of cartilage degeneration in transgenic animals expressing MMP-13* in joint tissue.

5 Mice harboring both the tet07-MMP-13* and CPE-tTA constructs (produced as described in Example 3 above) were maintained on doxycycline until adulthood (approximately 8 weeks postpartum).

Expression of MMP13* was first evaluated in hemizygous mice using RT-PCR to detect the transcripts. No expression of the transgene was observed in any of the lines in any of the tissues sampled, including brain, heart, liver, kidney, hindlimb, muscle, bone, or tongue.

To examine whether MMP-13* DNA in any of the double-transgenic lines was capable of being expressed, embryonic fibroblasts were prepared from these animals and transfected with a tTA expression plasmid (Gossen and Bujard, *Proc.Natl.Acad.Sci.USA* 89:5547, 1992). The transfection was done because the joint-specific type II collagen promoter regulating tTA expression (and thereby MMP-13* expression) in the transgenic animals might not be expected to function in embryonic fibroblasts.

For this purpose, wild-type females were mated to transgenic males harboring both the type II collagen promoter-linked tTA and Tet07-MMP-13* transgenes. On embryonic day 15, the females were sacrificed, and fibroblasts were prepared from the embryos (Graham et al., *Virol.* **52**:456, 1973; Lopata et al., *Nuc. Acid Res.* **12**:5707, 1984). The fibroblasts were cultured in DMEM containing 10% fetal bovine serum, and were transfected with the tTa expression plasmid using the calcium phosphate method. Forty-eight

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staining in the growth plate and in the articular cartilage could be seen (Figure 4), but the results differed among different lines of mice (see Table 1 below).

Table 1

Immunohistochemistry				
F1 Animal	Days off Dox	hMMP13 Ab	Type II Collagen Cleavage Fragments Ab	Loss of Safranin O Stain
Line 8	wt	-	-	not remarkable
Line 8	0 d	-	-	" "
	3 d	+	+	" "
	7 d	++	++	Mild
	14 d	+++	+++	Moderate
	wt	-	-	not remarkable
Line 6	30 d			Moderate
Line 8	30 d	+++	+++	Moderate
Line 42	30 d	+	-	not remarkable

To study the effect of MMP13* activity on cartilage in adult transgenic animals, mice were withdrawn from doxycycline for increasing times, after which they were sacrificed. Paraffin-embedded formaldehyde-fixed sections of decalcified cartilage were sectioned and stained with (i) hematoxylin and eosin and (ii) Safranin O followed by fast green (American Histo Labs, Gaithersburg MD). Peter et al., *J. Exp. Pathol.* **71**:19, 1990.

Control transgenic animals that lack MMP13* expression retain a significant amount of safranin O stain in both the articular cartilage as well as the growth plate of their patella (Figure 5, left panel). By contrast, transgenic animals from line 8 show a substantial loss of safranin O staining in their joints following doxycycline withdrawal. After seven days,

a mild reduction of safranin O staining is observed in the articular cartilage of the patella (Figure 5, middle panel), which progresses by day 14 to moderate loss of stain in articular cartilage as well as the growth plate (Figure 5, right panel). A significant loss of safranin O stain was also observed in the other joints including the cartilage of the tarsus and femur, as well as wrist and knuckle, indicating a reduced proteoglycan concentration in these areas compared to controls.

Example 6: Augmentation of the Development of Symptoms of Joint Degenerative Disease in MMP-13 Transgenic Mice

The following treatments are performed to enhance the symptoms of joint degeneration exhibited by the transgenic animals of the invention.

A group of transgenic mice are treated to induce expression of the transgenes at 4-12 weeks of age. Two to six weeks after induction, the mice are injected intraperitoneally with an inflammatory agent, including without limitation, lipopolysaccharide (10-100 μ g), zymosan (1-10 mg), the superantigen Staphylococcal Enterotoxin B (1-100 μ g), or TGF- β (1-10 μ g). Alternatively, the animals are injected intraarticularly with an inflammatory or chondrocyte function-modulating agent, including without limitation, lipopolysaccharide (1-100 ng), zymosan (50-250 μ g), papain (10-100 μ g), TGF- β (0.01-1 μ g), Bone Morphogenic Protein -2 (2-1000 ng), IL-1 (1-100 ng), TGF- α (10-200 ng), IGF (0.01-1 μ g), or FGF (0.01-1 μ g). Age- and sex-matched transgenic mice maintained under a regimen in which the transgenes are not expressed receive the same treatment and serve as controls.

The development of symptoms of degenerative joint disease is monitored by gross observation of joint swelling and function, and by histological evaluation of the joint at selected timepoints after exposure to the inflammatory agent.

5 The agents will induce an acute inflammatory response and/or transient loss of proteoglycan with a duration of less than one week. The acute inflammatory response and/or transient cartilage changes will upregulate gene expression in the chondrocytes, enhancing the expression of the transgene and increasing the levels of MMP-13 produced.

All patents, applications, articles, publications, and test methods mentioned above are hereby incorporated by reference in their entirety.

10 Many variations of the present invention will suggest themselves to those skilled in the art in light of the above detailed description. Such obvious variations are within the full intended scope of the appended claims.

Claims:

1 1. A transgenic non-human mammal or the progeny thereof having somatic
2 and germline cells which contain, in stably integrated form, a recombinant gene encoding a
3 polypeptide comprising an enzymatically active matrix-degrading enzyme, wherein said
4 recombinant gene is selectively expressed in chondrocytes of said mammal and said
5 expression results in pathological symptoms characteristic of cartilage-degenerative disease.

1 2. A transgenic animal or the progeny thereof having somatic and germline
2 cells which contain a stably integrated first recombinant gene encoding a polypeptide selected
3 from the group consisting of MMP-1, MMP-2, MMP-3, MMP-7, MMP-8, MMP-9, MMP-
4 10, MMP-13, MMP-14, MMP-15, MMP-16, MMP-17 and enzymatically active variants
5 thereof.

1 3. A transgenic animal as defined in claim 2, wherein said first recombinant
2 gene is selectively expressed in synovial chondrocytes of said animal.

1 4. A transgenic animal as defined in claim 2, wherein said first recombinant
2 gene encodes MMP-13.

1 5. A transgenic animal as defined in claim 4, wherein said MMP-13 is
2 human.

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1 14. A transgenic animal as defined in claim 12, wherein expression of said
2 second recombinant gene is under the control of a second regulatable promoter.

1 15. A transgenic animal as defined in claim 13, wherein said second
2 regulatable promoter comprises sequences derived from a type II collagen promoter that
3 confer selective expression of said second recombinant gene in joint tissues.

1 16. A transgenic mouse or the progeny thereof having somatic and germline
2 cells which contain in stably integrated form:

3 (i) a first recombinant gene comprising a sequence encoding a variant MMP-13
4 polypeptide comprising MMP-13*, wherein said sequence is operably linked to a tetO7
5 promoter; and

6 (ii) a second recombinant gene encoding a tTA protein operatively linked to
7 sequences derived from a type II collagen promoter.

1 17. A transgenic mouse as defined in claim 16 wherein expression of said
2 recombinant genes in joint tissue results in pathological symptoms characteristic of joint
3 degenerative disease.

1 18. An isolated nucleic acid encoding enzymatically active proMMP-13,
2 wherein said nucleic acid has a sequence selected from the group consisting of the sequence
3 depicted in SEQ ID NO:1, sequence-conservative mutants thereof, and function-conservative
4 mutants thereof.

24. A method for producing phenotypic changes associated with cartilage-degenerative disease in a mouse, comprising maintaining a mouse as defined in claim 16 for a predetermined time in the absence of tetracycline or biologically active analogues thereof.

8 (iii) monitoring development of said phenotypic indicators for a
9 predetermined time following administration of the composition; and

10 (iii) comparing the extent of the phenotypic indicators in the animal to
11 which the composition was administered relative to a control transgenic animal that had not
12 been exposed to the composition,
13 wherein any difference in the nature or extent of the phenotypic indicators indicates the
14 potential of the composition to counteract cartilage-degenerative disease.

1 27. A method for determining the potential of a composition to counteract
2 cartilage-degenerative disease, said method comprising:

3 (i) providing a transgenic animal as defined in claim 16 that had been
4 maintained in the presence of tetracycline or a tetracycline analogue to repress expression of
5 said first recombinant gene;

6 (ii) substantially simultaneously (a) administering to said animal a
7 known dose of said composition and (b) withdrawing said tetracycline;

8 (iii) monitoring development of phenotypic indicators of cartilage-
9 degenerative disease for a predetermined time following administration of the composition;
10 and

11 (iv) comparing the extent of the phenotypic indicators in the animal to
12 which the composition was administered relative to a control transgenic animal that had not
13 been exposed to the composition,

- 14 wherein any difference in the nature or extent of the indicators, or any difference in the time
15 required for the indicators to develop, indicates the potential of the composition to counteract
16 cartilage-degenerative disease.

Variable	Mean	SD	Min	Max
Age	22.14	2.14	18	28
Gender	0.48	0.50	0	1
Marital status	0.02	0.10	0	1
Religion	0.48	0.50	0	1
Education	12.14	1.14	10	14
Income	1.14	0.14	1	2
Health	1.14	0.14	1	2
Family size	3.14	0.14	2	4
Parental education	11.14	1.14	9	13
Parental income	1.14	0.14	1	2
Parental health	1.14	0.14	1	2
Parental family size	3.14	0.14	2	4
Parental marital status	0.02	0.10	0	1
Parental religion	0.48	0.50	0	1
Parental gender	0.48	0.50	0	1
Parental age	22.14	2.14	18	28
Parental education	12.14	1.14	10	14
Parental income	1.14	0.14	1	2
Parental health	1.14	0.14	1	2
Parental family size	3.14	0.14	2	4
Parental marital status	0.02	0.10	0	1
Parental religion	0.48	0.50	0	1
Parental gender	0.48	0.50	0	1
Parental age	22.14	2.14	18	28
Parental education	12.14	1.14	10	14
Parental income	1.14	0.14	1	2
Parental health	1.14	0.14	1	2
Parental family size	3.14	0.14	2	4
Parental marital status	0.02	0.10	0	1
Parental religion	0.48	0.50	0	1
Parental gender	0.48	0.50	0	1
Parental age	22.14	2.14	18	28
Parental education	12.14	1.14	10	14
Parental income	1.14	0.14	1	2
Parental health	1.14	0.14	1	2
Parental family size	3.14	0.14	2	4
Parental marital status	0.02	0.10	0	1
Parental religion	0.48	0.50	0	1
Parental gender	0.48	0.50	0	1
Parental age	22.14	2.14	18	28
Parental education	12.14	1.14	10	14
Parental income	1.14	0.14	1	2
Parental health	1.14	0.14	1	2
Parental family size	3.14	0.14	2	4
Parental marital status	0.02	0.10	0	1
Parental religion	0.48	0.50	0	1
Parental gender	0.48	0.50	0	1
Parental age	22.14	2.14	18	28
Parental education	12.14	1.14	10	14
Parental income	1.14	0.14	1	2
Parental health	1.14	0.14	1	2
Parental family size	3.14	0.14	2	4
Parental marital status	0.02	0.10	0	1
Parental religion	0.48	0.50	0	1
Parental gender	0.48	0.50	0	1
Parental age	22.14	2.14	18	28
Parental education	12.14	1.14	10	14
Parental income	1.14	0.14	1	2
Parental health	1.14	0.14	1	2
Parental family size	3.14	0.14	2	4
Parental marital status	0.02	0.10	0	1
Parental religion	0.48	0.50	0	1
Parental gender	0.48	0.50	0	1
Parental age	22.14	2.14	18	28
Parental education	12.14	1.14	10	14
Parental income	1.14	0.14	1	2
Parental health	1.14	0.14	1	2
Parental family size	3.14	0.14	2	4
Parental marital status	0.02	0.10	0	1
Parental religion	0.48	0.50	0	1
Parental gender	0.48	0.50	0	1
Parental age	22.14	2.14	18	28
Parental education	12.14	1.14	10	14
Parental income	1.14	0.14	1	2
Parental health	1.14	0.14	1	2
Parental family size	3.14	0.14	2	4
Parental marital status	0.02	0.10	0	1
Parental religion	0.48	0.50	0	1
Parental gender	0.48	0.50	0	1
Parental age	22.14	2		

M:\0630\0D532\RG1795

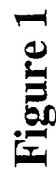


Figure 1

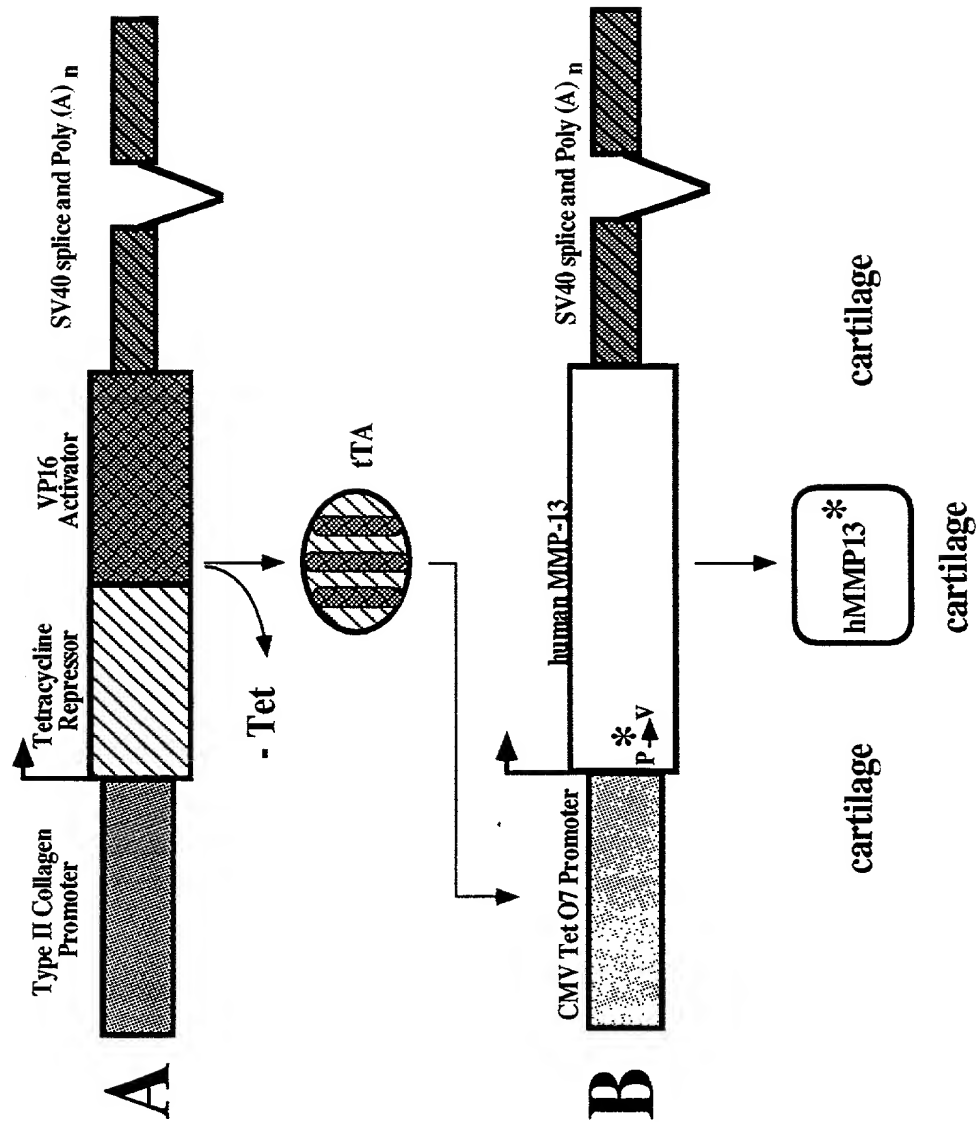


Figure 2

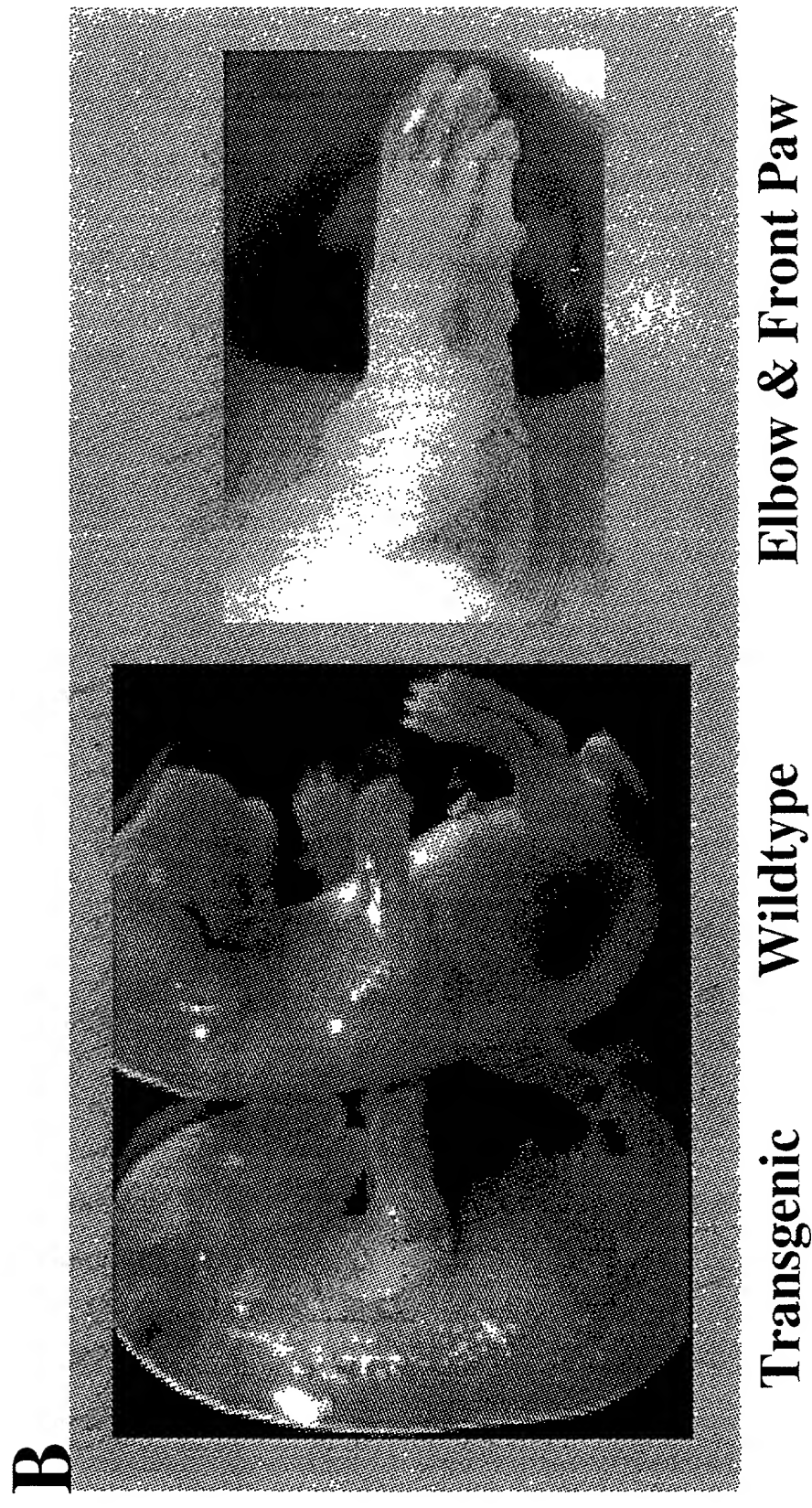
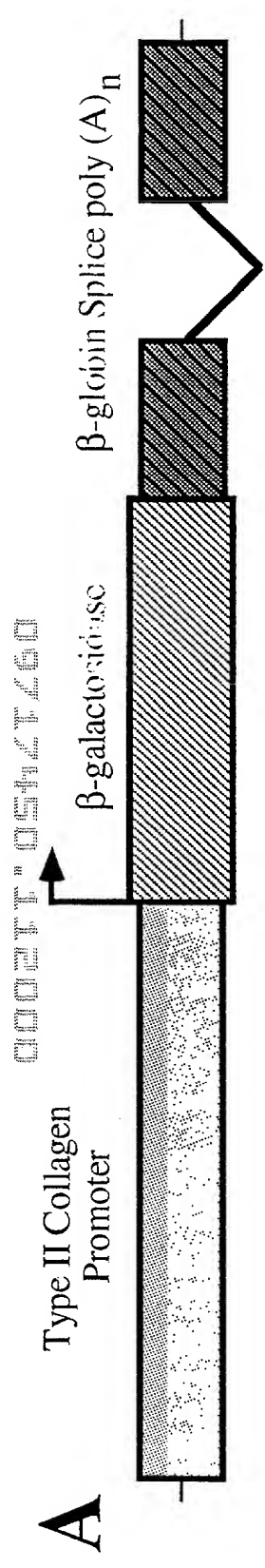


Figure 3

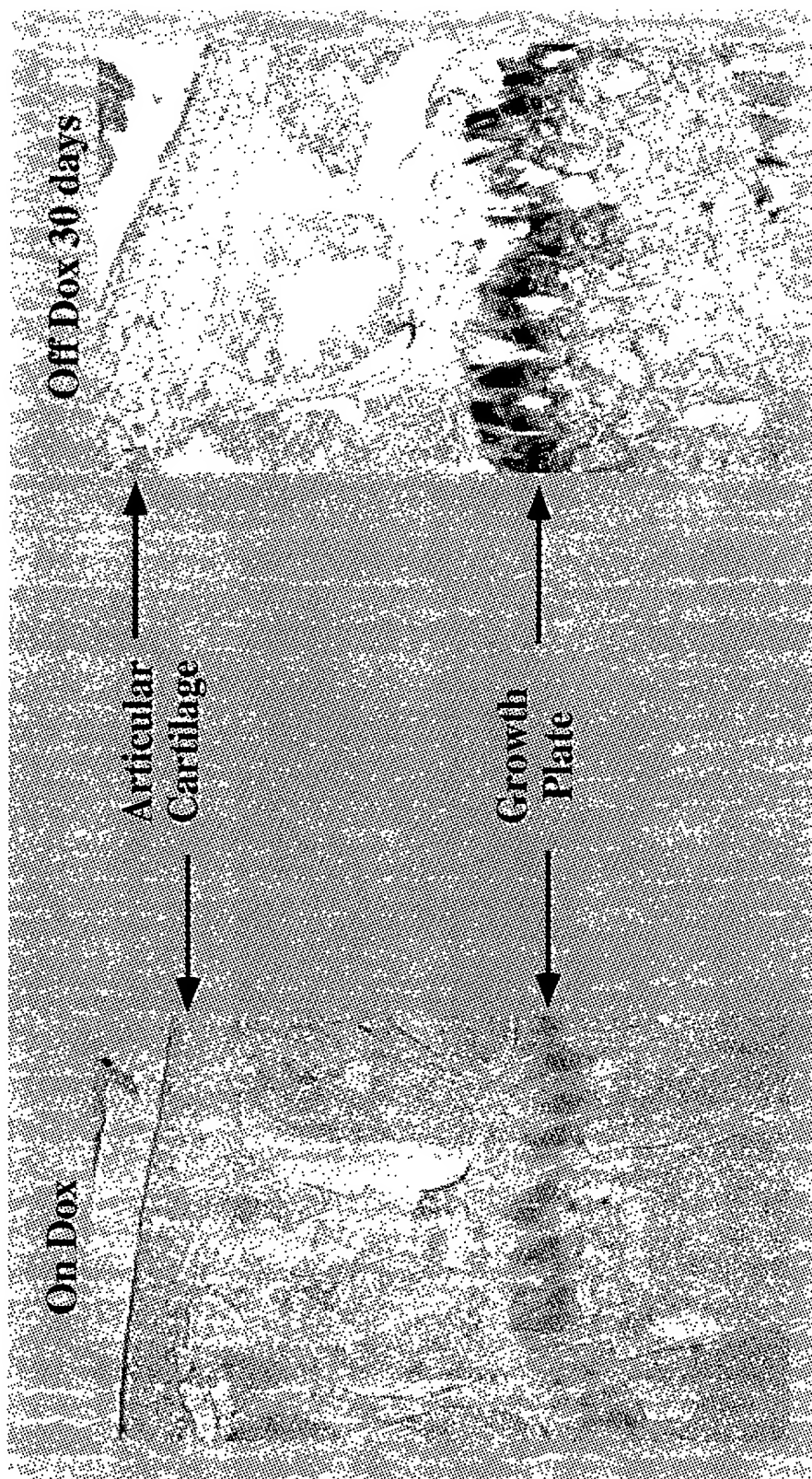


Figure 4

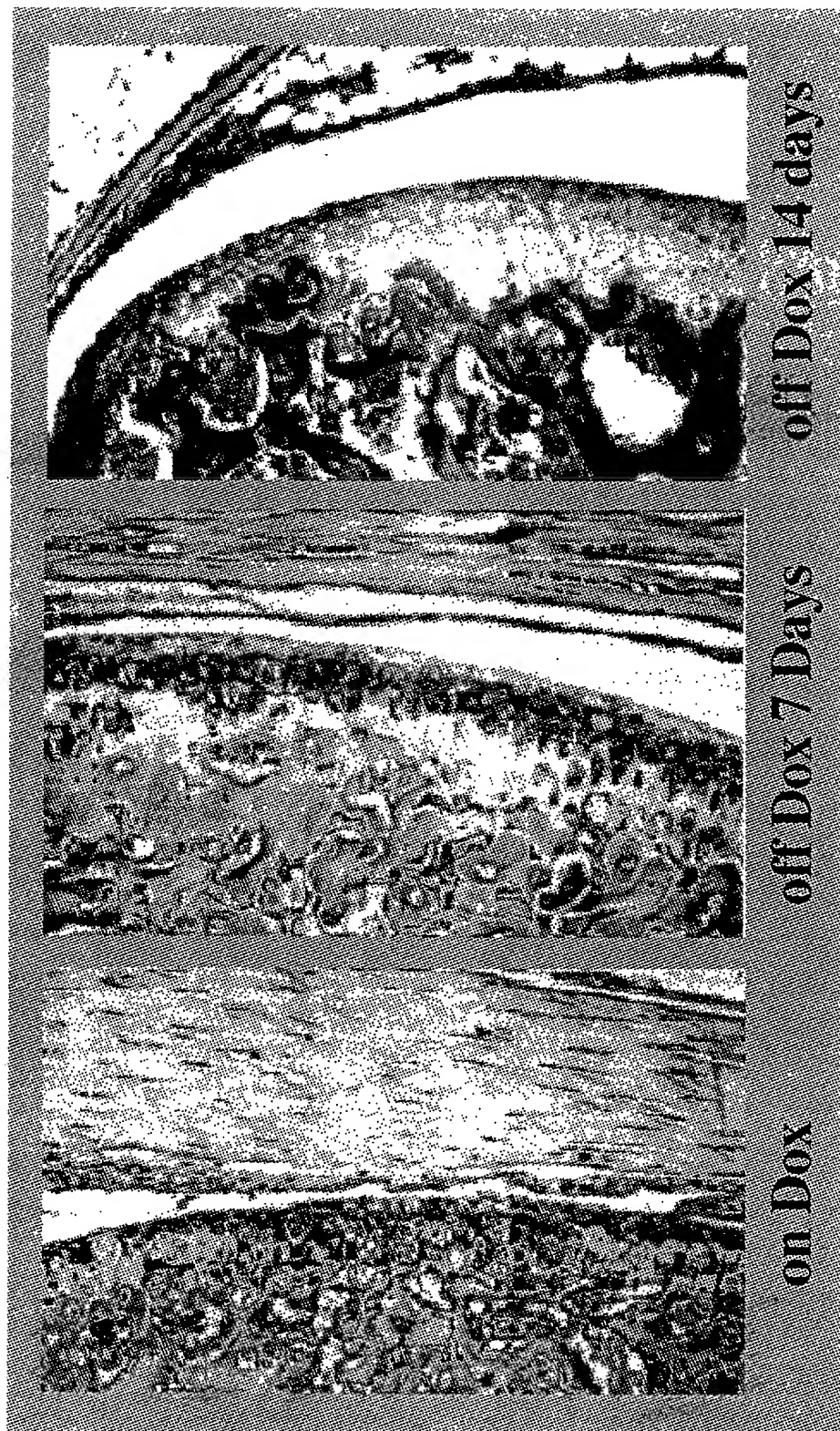


Figure 5

**DECLARATION
AND POWER OF ATTORNEY
Original Application**

As a below named inventor, I declare that the information given herein is true, that I believe that I am the original, first and sole inventor if only one name is listed at 1 below, or a joint inventor if plural inventors are named below, of the invention entitled:

TRANSGENIC ANIMAL MODEL FOR DEGENERATIVE DISEASES OF CARTILAGE

which is described and claimed in the attached specification,

that I do not know and do not believe that the same was ever known or used in the United States of America before my or our invention thereof or patented or described in any printed publication in any country before my or our invention thereof, or more than one year prior to this application, or in public use or on sale in the United States of America more than one year prior to this application, that the invention has not been patented or made the subject of an inventor's certificate issued before the date of this application in any country foreign to the United States of America on an application filed by me or my legal representatives or assigns more than twelve months prior to this application, that I acknowledge my duty to disclose information of which I am aware which is material to patentability in accordance with 37 CFR §1.56. I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above. I hereby claim the priority benefits under 35 U.S.C. 119 of any application(s) for patent or inventor's certificate listed below. All foreign applications for patent or inventor's certificate on this invention filed by me or my legal representatives or assigns prior to the application(s) of which priority is claimed are also identified below.

POWER OF ATTORNEY:

As a named inventor, I hereby appoint the following attorney(s) and/or agents(s) to prosecute this application and transact all business in the Patent and Trademark office connected therewith:

Gordon D. Coplein #19,165, William F. Dudine, Jr. #20,569, Michael J. Sweedler #19,937, S. Peter Ludwig #25,351, Paul Fields #20,298, Harold E. Wurst #22,183, Joseph B. Lerch #26,936, Melvin C. Garner #26,272, Ethan Horwitz #27,646, Beverly B. Goodwin #28,417, Adda C. Gogoris #29,714, Martin E. Goldstein #20,869, Bert J. Lewen #19,407, Henry Sternberg #22,408, Robert A. Green #28,301, Peter C. Schechter #31,662, Robert Schaffer #31,194, David R. Francescani #25,159, Robert C. Sullivan, Jr. #30,499, Ira J. Levy #35,587, Joseph R. Robinson #33,448

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and Egon E. Berg #21,117, Steven H. Flynn # 29,639, Adley F. Mandel #26,942, Ronald W. Alice #27,609, Gale F. Matthews #32,269, Milagros A. Cepeda #33,365, Alan M. Gordon #30,637, Elizabeth M. Barnhard #31,088, Andrea C. Walsh # 34,988, and Darryl L. Webster #34,276

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FULL NAME AND RESIDENCE OF INVENTOR 1

LAST NAME: NEUHOLD FIRST NAME: Lisa MIDDLE NAME: Ann

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COUNTRY OF CITIZENSHIP: USA

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FULL NAME AND RESIDENCE OF INVENTOR 2

LAST NAME: KILLAR FIRST NAME: Loran MIDDLE NAME: Marie

CITY: Newtown STATE OR FOREIGN COUNTRY: Pennsylvania COUNTRY OF

CITIZENSHIP: USA

POST OFFICE ADDRESS: 206 Farmview Drive CITY: Newtown

STATE OR COUNTRY: Pennsylvania ZIP CODE: 18940

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

000217 054760

SIGNATURE OF INVENTOR 1: Lia A. Naldol DATED: 12/18/97

United States of America)
State of: N.J.) S.S.:
County of: Middlesex

MARIE ARCARO
MY COMMISSION EXPIRES Marie Arcaro
ON JUNE 9, 1999

Sworn to and subscribed before me this 18th day of December, 1997.

SIGNATURE OF INVENTOR 2: Lora Marie Hill DATED: 12/18/97

United States of America)
State of: N.J.) S.S.:
County of: Middlesex

Sworn to and subscribed before me this 18th day of December, 1997.

MARIE ARCARO
MY COMMISSION EXPIRES
ON JUNE 9, 1999

Marie Arcaro

(D&D Forms/PTO-21)
EV. 12/87

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Neuhold, Lisa
Killar, Loran
- (ii) TITLE OF THE INVENTION: TRANSGENIC ANIMAL MODEL FOR
DEGENERATIVE DISEASES OF CARTILAGE
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Darby & Darby PC
(B) STREET: 805 Third Avenue
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/994,689
(B) FILING DATE: 1997-12-19
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Green, Reza
(B) REGISTRATION NUMBER: 38,475
(C) REFERENCE/DOCKET NUMBER: 0630/0D532
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(A) TELEPHONE: 212-527-7700
(B) TELEFAX: 212-753-6237
(C) TELEX: 236687

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	His	Pro	Gly	Val	Leu	Ala	Ala	Phe	Leu	Phe	Leu	Ser	Trp	Thr	His
1				5					10					15	
Cys	Arg	Ala	Leu	Pro	Leu	Pro	Ser	Gly	Gly	Asp	Glu	Asp	Asp	Leu	Ser
			20					25					30		
Glu	Glu	Asp	Leu	Gln	Phe	Ala	Glu	Arg	Tyr	Leu	Arg	Ser	Tyr	Tyr	His
		35					40					45			
Pro	Thr	Asn	Leu	Ala	Gly	Ile	Leu	Lys	Glu	Asn	Ala	Ala	Ser	Ser	Met
	50					55					60				
Thr	Glu	Arg	Leu	Arg	Glu	Met	Gln	Ser	Phe	Phe	Gly	Leu	Glu	Val	Thr
65					70					75				80	
Gly	Lys	Leu	Asp	Asp	Asn	Thr	Leu	Asp	Val	Met	Lys	Lys	Pro	Arg	Cys
			85						90					95	
Gly	Val	Val	Asp	Val	Gly	Glu	Tyr	Asn	Val	Phe	Pro	Arg	Thr	Leu	Lys
			100					105					110		
Trp	Ser	Lys	Met	Asn	Leu	Thr	Tyr	Arg	Ile	Val	Asn	Tyr	Thr	Pro	Asp
		115					120					125			
Met	Thr	His	Ser	Glu	Val	Glu	Lys	Ala	Phe	Lys	Lys	Ala	Phe	Lys	Val
	130					135					140				
Trp	Ser	Asp	Val	Thr	Pro	Leu	Asn	Phe	Thr	Arg	Leu	His	Asp	Gly	Ile
145					150					155				160	
Ala	Asp	Ile	Met	Ile	Ser	Phe	Gly	Ile	Lys	Glu	His	Gly	Asp	Phe	Tyr
			165						170					175	
Pro	Phe	Asp	Gly	Pro	Ser	Gly	Leu	Leu	Ala	His	Ala	Phe	Pro	Pro	Gly
			180				185						190		
Pro	Asn	Tyr	Gly	Gly	Asp	Ala	His	Phe	Asp	Asp	Asp	Glu	Thr	Trp	Thr
	195					200						205			
Ser	Ser	Ser	Lys	Gly	Tyr	Asn	Leu	Phe	Leu	Val	Ala	Ala	His	Glu	Phe
	210					215					220				
Gly	His	Ser	Leu	Gly	Leu	Asp	His	Ser	Lys	Asp	Pro	Gly	Ala	Leu	Met
225				230						235				240	
Phe	Pro	Ile	Tyr	Thr	Tyr	Thr	Gly	Lys	Ser	His	Phe	Met	Leu	Pro	Asp
			245						250					255	
Asp	Asp	Val	Gln	Gly	Ile	Gln	Ser	Leu	Tyr	Gly	Pro	Gly	Asp	Glu	Asp
			260				265						270		
Pro	Asn	Pro	Lys	His	Pro	Lys	Thr	Pro	Asp	Lys	Cys	Asp	Pro	Ser	Leu
	275					280						285			
Ser	Leu	Asp	Ala	Ile	Thr	Ser	Leu	Arg	Gly	Glu	Thr	Met	Ile	Phe	Lys
	290					295					300				
Asp	Arg	Phe	Phe	Trp	Arg	Leu	His	Pro	Gln	Gln	Val	Asp	Ala	Glu	Leu
305					310					315				320	
Phe	Leu	Thr	Lys	Ser	Phe	Trp	Pro	Glu	Leu	Pro	Asn	Arg	Ile	Asp	Ala
			325						330					335	

Ala Tyr Glu His Pro Ser His Asp Leu Ile Phe Ile Phe Arg Gly Arg
340 345 350
Lys Phe Trp Ala Leu Asn Gly Tyr Asp Ile Leu Glu Gly Tyr Pro Lys
355 360 365
Lys Ile Ser Glu Leu Gly Leu Pro Lys Glu Val Lys Lys Ile Ser Ala
370 375 380
Ala Val His Phe Glu Asp Thr Gly Lys Thr Leu Leu Phe Ser Gly Asn
385 390 395 400
Gln Val Trp Arg Tyr Asp Asp Thr Asn His Ile Met Asp Lys Asp Tyr
405 410 415
Pro Arg Leu Ile Glu Glu Asp Phe Pro Gly Ile Gly Asp Lys Val Asp
420 425 430
Ala Val Tyr Glu Lys Asn Gly Tyr Ile Tyr Phe Phe Asn Gly Pro Ile
435 440 445
Gln Phe Glu Tyr Ser Ile Trp Ser Asn Arg Ile Val Arg Val Met Pro
450 455 460
Ala Asn Ser Ile Leu Trp Cys
465 470

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTCGAGTTTA	CCACTCCCTA	TCAGTGATAG	AGAAAAGTGA	AAGTCGAGTT	TACCACTCCC	60
TATCAGTGAT	AGAGAAAAGT	GAAAGTCGAG	TTTACCACTC	CCTATCAGTG	ATAGAGAAAA	120
GTGAAAGTCG	AGTTTACCAC	TCCCTATCAG	TGATAGAGAA	AAGTGAAAGT	CGAGTTTACC	180
ACTCCCTATC	AGTGATAGAG	AAAAGTGAAA	GTCGAGTTTA	CCACTCCCTA	TCAGTGATAG	240
AGAAAAGTGA	AAGTCGAGTT	TACCACTCCC	TATCAGTGAT	AGAGAAAAGT	GAAAGTCGAG	300
CTCGGTACCC	GGGTCGAGTA	GGCGTGTACG	GTGGGAGGCC	TATATAAGCA	GAGCTCGTTT	360
AGTGAACCGT	CAGATCGCCT	GGAGACGCCA	TCCACGCTGT	TTTGACCTCC	ATAGAAGACA	420
CCGGGACCGA	TCCAGCCTCC	GCGGCCCCGA	ATTAGCTTGA	TATCGAATTC		470

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTACCACTA	GTAAGCTTAG	ATCCACTGTC	TGGGATTATA	TCAGGACAAC	CGAAGCCTGG	60
------------	------------	------------	------------	------------	------------	----

AAAGTGTATT	AGGTAGAGCA	TTTTCTTCCA	CGTGTTTGGG	CACGTTTCCG	ACAGCTAGGA	120
TTCCAGCTCT	GTCTTTGTAT	GTTACAGACT	GTAAATCAAT	CGCAGGTGAA	ACTGTTTGGG	180
CAGTAGGTGG	GGATCAAAGA	CCCTCCGCCC	GTGAGACTCT	AGGCGCTTTC	CCCTGCCACC	240
AGCCTGTCTC	CAGAGATGCT	CTGGAAGGAG	GCGGGCCCCG	GCGGTCTTTC	TGCTCTTTAG	300
CGTGGCGGAC	GCGGCGGCGG	GGGCAGGGCT	GGAGCAGAGA	GCGCTGCAGT	GATAGAACTT	360
TCTGACCCCG	CTGCGCAGGG	CGGCAGGGTG	GCAGGGTGCC	AGGGTGGCGA	GCTAAGCCAG	420
AGCCGAACGC	TGGAGCTCTG	GGAGGAACAT	CGAAGGTTTG	TATGTGGTCT	GAGATCGGCC	480
TGACTATATT	TTTTTGTCTT	AAATTTGCAA	GCACACACCC	ACAAAGCTGC	GGTCTTGACC	540
GGTATTCTTT	ATAGAGCGCA	ATGGAGTGAG	CTGAGTGTCT	AAACGATTTT	CCTAATTCAT	600
CTGATAGCAG	AGGCGCTCTC	CTAATTGGCG	AAGAGCTGCC	TCATGTCCGC	AACTTTTTTG	660
CAGAGTGAAT	TCCACAGCTT	TGTGTGTGTG	TGTGGGGGGG	GGTGTAAGGG	GTGTCTAAAA	720
CTTTCGGTCT	CCTACTATT	TGTATCTCGA	CCGGTTGGTT	TTACACCCCG	GCTCATCTCA	780
TCAACGCAAA	CACCCCCACT	CTCCTATGGA	CCCAAGGACC	TGACGTGGGG	GAAGGTGGAC	840
ATTAGGAATG	TCAGAAACCT	AGAGTCCACG	CTCCTCCTCT	CCATCTTTCC	ACGAGTTTGG	900
GAAACTTCTT	GGCTGCGAAG	ACTTTGACCC	ACATCTGCAT	TTCTCAGCCC	CAGCTTCCAA	960
AAGTGCTGCA	GGTTCGGGAG	GGGAGACCTC	AGTCCTCCTT	TGTGAGGCTT	GTTTGC GTTG	1020
AGGGATTGGC	AGCGATGGCT	TCCAGATGGG	CTGAAACCC	GCCCGTATTT	ATTTAAACTG	1080
GTTCTCTCGT	GAGAGCTGTG	AATCGGGCTC	TGTATGCGCT	CGAGAAAAGC	CCCATTCATG	1140
AGAGGCAAGG	CCCAGTGGGT	CCCCCGACT	CCCCGACCCC	CCTCTCCCAC	AATATATCCC	1200
CCCTCCCTGT	GCCCGCCTGC	CGCCACCTCC	CGGGCTCCGG	CCCCGCGCGC	AGCGGCGACG	1260
AAGCAACACA	GTTCCCCGAA	AGAGGTAGCT	TTTTAATTGG	CCAGCCACAA	AGAATCACTT	1320
ATGCCGCACG	GCGGTAACGA	GGGGAACCGG	ATCGGGCGGC	CAGGATGCTA	TCTGTGTAGC	1380
CCTTTTCGTG	CCACAATTAG	GGTGGTGCTG	GCTTCCTCCG	ACCGCACCTA	GGCGATCTGG	1440
TTACACTGTT	GGCTCCTTTC	TTGGGCAGTC	ATTTAATCCT	ACTTTTTTACT	CTACGAATGT	1500
CTGTCTGATG	GAGGGCTGTG	TCCGGAGCCC	CATCCACAAA	GAGTCAGCCA	GCAGCTCTCA	1560
CACCCGGCTG	GATCTCATAT	GGTGCACCTC	CAGTACAATC	TGCTCTGATG	CCGCATAGTT	1620
AAGCCAGCCA	AGCTAGCTTG	CGCAAGCTAG	CTTGCGATCC	GTAAAAATGT	GTGAGAGTTA	1680
CAAAATGTCT	TCCGGGCTAA	GATCCGACAG	CCATGGTCCA	AAGAAGACTT	CGGCACTGCA	1740
GACTTAAAAC	CAGCTTTCTA	GCAGAGGCAG	AAGGATCTAG	AGCCAAAGGC	AAAGACTTGA	1800
ATAGGCTGGG	AAGATGCAAG	AATGGCATT	TACATAAAGA	ACACTCTCTC	CTTTTCCAGC	1860
CAGCACACTT	GCATAGAAAT	TAAGTTTTAC	ACTTGAAGTT	CTTTGTTTCC	ATCCTGAGAA	1920
GCTCCAAAGT	CTGAGGTGGT	GTGGTATGCT	GGGTAATTCT	CCCCACCCCC	CAACATTCCC	1980
TGGGGGTTCC	ATGGGGGTAG	CTTCTCCCAA	GGACTTCCAG	CGGCAACACA	GAAATCCCAC	2040
TTTCGAGACAA	AGGAGTTACT	GCTTAAATCA	GGCCCTAATT	TCCAAGGTTT	CCTTTGCTTA	2100
AAGTTCCCTA	GAGGACCATC	TCACTTCTAA	AGAAAAGGTG	TATTCGGGGA	CCCATCCTCA	2160
ACCTCCTTGT	TATGGAAGGA	GACTTCGGGA	ACAGAGCAAG	GGCTGAGCCT	CCGGCAGTTT	2220
GGGGTAAGGT	TGGGGTTGGG	GGGAGCAAGG	AAGGCAAGTG	AGGCTGGAGG	CCCAGGGATA	2280
GGGGAAGATG	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTC	TCGGGGATGG	2340
TGGTGGTGGA	CAACTAGGAA	ACTCTGGCGC	TTTCTCCTCC	CCTCACAAAA	CTGAGTCCAG	2400
CTGGAGCCGC	CTCCAGACTC	TCTGGCCAGG	GCCTCAGAGT	GGTCAACAGT	CCCTGGCCAG	2460
CGTTGTCTCT	TCCAGGCTAA	GGGCACCCAC	TCCCCTGGAG	ATTCTGAAC	CTGGGCCAGG	2520
AAGAGCCGAA	TTAGACAAGT	GTCTCCAATC	CGGCTGCGTG	CGGATTTTGT	TGCGGTGTCC	2580
CTCGGTTGTC	TGCAGTTCCT	TTAGTCCCTT	CCCTGGCCTG	CCCCTTACAC	CTCCACACAG	2640
GTCCCCCTCT	GTGTAGGAAT	ACACCAGACC	CTCTCTTAGC	CACACACACC	TCCAGTCCCC	2700
CGTCTACCTA	GATTTTTTTC	ATAGCTAGTT	GGATGGGGGA	TGGGTTAGGG	AGGCTGGGTT	2760
TGCGAGCCTC	CAGGTGGGAG	TTACCCGACA	GGTACTCCGC	AAAGGAGCTG	GAAGGCAGGT	2820
CTGGAAAAC	GTCCCCCAGA	TTTAGGATTC	TGGGCAGCTT	CCATCAGCTT	ATACTTTGGC	2880
TCCCCCGCCC	CCTAAACTCC	CCATCCCCAC	CTTCCTTTCT	CCCGTTACTT	CGTCCTCCCT	2940
CGCCTTTCCA	GCCTTGAGTC	TAAAGCTCCA	TGCTTATGCC	TCTGCAAACA	ACCCCTCCC	3000
TTCTAACCCC	AGCAGAACTC	CGAGGAAAGG	GGCCGGAGGC	CCCCCTTCTC	GCCTGTGGTT	3060
AGAGGGGGCA	GTGTGGCAGT	CCCAAGTGGG	GGCGACCGGA	GGCCGTCTCG	GTGCCCCGCC	3120

CGATCAGGCC	ACTGGGCACA	TCGGGGGCGG	GAAGCTGGGC	TCACCAAAGG	GGCGACTGGC	3180
CTTGGCAGGT	GTGGGCTCTG	GTCCGGCCTG	GGCAGGCTCC	GGGGGCGGGG	TCTCAGGTTA	3240
CAGCCCCGCG	GGGGGCTGGG	GGGCGGCCCG	CGGTTTGGGC	TGGTTTGCCA	GCCTTTGGAG	3300
CGACCGGGAG	CATATAACCG	GAGCCTCTGC	TGGGAGAAGA	CGCAGAGCGC	CGCTGGGCTG	3360
CCGGGTCTCC	TGCTCTCTCC	TCCTGCTCCT	AGAGCCTCCT	GCATGAGGGC	GCGGTAGAGA	3420
CCCGGACCCG	CTCCGTGCTC	TGCCGCCTCG	CCGAGCTTCG	CCCGCAAGCT	GGGGAATTC	3479

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro Arg Cys Gly Val Pro Asp Val
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCCAAGAT	GCGGGGTTGT	CGATGTGGGT	GAATACAAT	39
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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAAAAAGCCA	AGATGCGGGG	GTCCTGATGT	GGGTGAATAC	40
------------	------------	------------	------------	----

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTACCACTA	GTAAGCTTAG	ATCTCATATG	GTCGACCCCG	GGAATTCCT	GCAGGGATCC	60
TCTAGAAGTA	CTCCATGGGT	ATACATCGAT	GCGGCCGC			98

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCGAGTTTA	CCACTCCCTA	TCAGTGATAG	AGAAAAGTGA	AAGTCGAGTT	TACCACTCCC	60
TATCAGTGAT	AGAGAAAAGT	GAAAGTCGAG	TTTACCACTC	CCTATCAGTG	ATAGAGAAAA	120
GTGAAAGTCG	AGTTTACCAC	TCCCTATCAG	TGATAGAGAA	AAGTGAAAGT	CGAGTTTACC	180
ACTCCCTATC	AGTGATAGAG	AAAAGTGAAA	GTCGAGTTTA	CCACTCCCTA	TCAGTGATAG	240
AGAAAAGTGA	AAGTCGAGTT	TACCACTCCC	TATCAGTGAT	AGAGAAAAGT	GAAAGTCGAG	300
CTCGGTACCC	GGGTCGAGTA	GGCGTGTACG	GTGGGAGGCC	TATATAAGCA	GAGCTCGTTT	360
AGTGAACCGT	CAGATCGCCT	GGAGACGCCA	TCCACGCTGT	TTTGACCTCC	ATAGAAGACA	420
CCGGGACCGA	TCCAGCCTCC	GCGGCCCCGA	ATTAGCTTGA	TATCGAATTC	GAGCTCGGTA	480
CCCGGGGATC	CTCTAGACAA	GATGCATCCA	GGGGTCCTGG	CTGCCTTCCT	CTTCTTGAGC	540
TGGACTCATT	GTCGGGCCCT	GCCCCTTCCC	AGTGGTGGTG	ATGAAGATGA	TTTGTCTGAG	600
GAAGACCTCC	AGTTTGCAGA	GCGCTACCTG	AGATCATACT	ACCATCCTAC	AAATCTCGCG	660
GGAATCCTGA	AGGAGAATGC	AGCAAGCTCC	ATGACTGAGA	GGCTCCGAGA	AATGCAGTCT	720
TTCTTCGGCT	TAGAGGTGAC	TGGCAAACCT	GACGATAACA	CCTTAGATGT	CATGAAAAAG	780
CCAAGATGCG	GGGTTGTCGA	TGTGGGTGAA	TACAATGTTT	TCCCTCGAAC	TCTTAAATGG	840
TCCAAAATGA	ATTTAACCTA	CAGAATTGTG	AATTACACCC	CTGATATGAC	TCATTCTGAA	900
GTCGAAAAGG	CATTCAAAAA	AGCCTTCAAA	GTTTGGTCCG	ATGTAACTCC	TCTGAATTTT	960
ACCAGACTTC	ACGATGGCAT	TGCTGACATC	ATGATCTCTT	TTGGAATTAA	GGAGCATGGC	1020
GACTTCTACC	CATTTGATGG	GCCCTCTGGC	CTGCTGGCTC	ATGCTTTTCC	TCCTGGGCCA	1080
AATTATGGAG	GAGATGCCCA	TTTTGATGAT	GATGAAACCT	GGACAAGTAG	TTCCAAAGGC	1140
TACAACTTGT	TTCTTGTTGC	TGCGCATGAG	TTCGGCCACT	CCTTAGGTCT	TGACCACTCC	1200
AAGGACCCTG	GAGCACTCAT	GTTTCCTATC	TACACCTACA	CCGGCAAAAG	CCACTTTATG	1260
CTTCCTGATG	ACGATGTACA	AGGGATCCAG	TCTCTCTATG	GTCCAGGAGA	TGAAGACCCC	1320
AACCCTAAAC	ATCCAAAAAC	GCCAGACAAA	TGTGACCCTT	CCTTATCCCT	TGATGCCATT	1380
ACCAGTCTCC	GAGGAGAAAC	AATGATCTTT	AAAGACAGAT	TCTTCTGGCG	CCTGCATCCT	1440
CAGCAGGTTG	ATGCGGAGCT	GTTTTTAACG	AAATCATTTT	GGCCAGAACT	TCCCAACCGT	1500
ATTGATGCTG	CATATGAGCA	CCCTTCTCAT	GACCTCATCT	TCATCTTCAG	AGGTAGAAAA	1560
TTTTGGGCTC	TTAATGGTTA	TGACATTCTG	GAAGGTTATC	CCAAAAAAT	ATCTGAACTG	1620
GGTCTTCCAA	AAGAAGTTAA	GAAGATAAGT	GCAGCTGTTC	ACTTTGAGGA	TACAGGCAAG	1680

ACTCTCCTGT	TCTCAGGAAA	CCAGGTCTGG	AGATATGATG	ATACTAACCA	TATTATGGAT	1740
AAAGACTATC	CGAGACTAAT	AGAAGAAGAC	TTCCCAGGAA	TTGGTGATAA	AGTAGATGCT	1800
GTCTATGAGA	AAAATGGTTA	TATCTATTTT	TTCAACGGAC	CCATACAGTT	TGAATACAGC	1860
ATCTGGAGTA	ACCGTATTGT	TCGCGTCATG	CCAGCAAATT	CCATTTTGTG	GTGTTAAGTG	1920
TCTTTTTTAAA	AATTGTTATT	TAAATCCTGA	AGAGCATTTG	GGGTAATACT	TCCAGAAGTG	1980
CGGGGTAGGG	GAAGAAGAGC	TATCAGGAGA	AAGCTCTAGT	TCTAGAGGGC	CCTATTCTAT	2040
AGTGTACACT	AAATGCTAGA	GGATCTTTGT	GAAGGAACCT	TACTTCTGTG	GTGTGACATA	2100
ATTGGACAAA	CTACCTACAG	AGATTTAAAG	CTCTAAGGTA	AATATAAAAT	TTTTAAGTGT	2160
ATAATGTGTT	AAACTACTGA	TTCTAATTGT	TTGTGTATTT	TAGATTCCAA	CCTATGGAAC	2220
TGATGAATGG	GAGCAGTGGT	GGAATGCCTT	TAATGAGGAA	AACCTGTTTT	GCTCAGAAGA	2280
AATGCCATCT	AGTGATGATG	AGGCTACTGC	TGACTCTCAA	CATTCTACTC	CTCCAAAAAA	2340
GAAGAGAAAG	GTAGAAGACC	CCAAGGACTT	TCCTTCAGAA	TTGCTAAGTT	TTTTGAGTCA	2400
TGCTGTGTTT	AGTAATAGAA	CTCTTGCTTG	CTTTGCTATT	TACACCACAA	AGGAAAAAGC	2460
TGCACTGCTA	TACAAGAAAA	TTATGGAAAA	ATATTTGATG	TATAGTGCCT	TGACTAGAGA	2520
TCATAATCAG	CCATACCACA	TTTGTAGAGG	TTTTACTTGC	TTTAAAAAAC	CTCCACACC	2580
TCCCCCTGAA	CCTGAAACAT	AAAATGAATG	CAATTGTTGT	TGTTAACTTG	TTTATTGCAG	2640
CTTATAATGG	TTACAAATAA	AGCAATAGCA	TCACAAATTT	CACAAATAAA	GCATTTTTTT	2700
CACTGCATTC	TAGTTGTGGT	TTGTCCAAAC	TCATCAATGT	ATCTTATCAT	GTCTGGATCA	2760
TCCCGCCATG	GGTATACATC	GATGCGGCCG	CC			2792

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGTACCACTA	GTAAGCTTAG	ATCCACTGTC	TGGGATTATA	TCAGGACAAC	CGAAGCCTGG	60
AAAGTGTATT	AGGTAGAGCA	TTTTCTTCCA	CGTGTTTGGG	CACGTTTCCG	ACAGCTAGGA	120
TTCCAGCTCT	GTCTTTGTAT	GTTACAGACT	GTAAATCAAT	CGCAGGTGAA	ACTGTTTGGA	180
CAGTAGGTGG	GGATCAAAGA	CCCTCCGCCC	GTGAGACTCT	AGGCGCTTTC	CCCTGCCACC	240
AGCCTGTCTC	CAGAGATGCT	CTGGAAGGAG	GCGGGCCCCG	GCGGTCTTTC	TGCTCTTTAG	300
CGTGGCGGAC	GCGGCGGCGG	GGGCAGGGCT	GGAGCAGAGA	GCGCTGCAGT	GATAGAAGTT	360
TCTGACCCCG	CTGCGCAGGG	CGGCAGGGTG	GCAGGGTGGC	AGGGTGGCGA	GCTAAGCCAG	420
AGCCGAACGC	TGGAGCTCTG	GGAGGAACAT	CGAAGTGTTT	GTATGTGGTC	TGAGATCGGC	480
CTGACTATAT	TTTTTTGTCC	TAAATTTGCA	AGCACACACC	CACAAAGCTG	CGGTCTTGAC	540
CGGTATTCTT	TATAGAGCGC	AATGGAGTGA	GCTGAGTGTC	TAAACGATTT	CCCTAATTCA	600
TCTGATAGCA	GAGGCGCTCT	CCTAATTGGC	GAAGAGCTGC	CTCATGTCCG	CAACTTTTTG	660
GCAGAGTGAA	TTCCACAGCT	TTGTGTGTGT	GTGTGGGGGG	GGGTGTAAGG	GGTGTCTAAA	720
ACTTTCGGTC	TCCTACTATT	CTGTATCTCG	ACCGGTTGGT	TTTACACCCC	GGCTCATCTC	780
ATCAACGCAA	ACACCCCCAC	TCTCCTATGG	ACCCAAGGAC	CTGACGTGGG	GGAAGGTGGA	840
CATTAGGAAT	GTCAGAAACC	TAGAGTCCAC	GCTCCTCCTC	TCCATCTTTC	CACGAGTTTG	900
GGAAACTTCT	TGGCTGCGAA	GACTTTGACC	CACATCTGCA	TTTCTCAGCC	CCAGCTTCCA	960
AAAGTGCTGC	AGGTTTCGGGA	GGGGAGACCT	CAGTCCTCCT	TTGTGAGGCT	TGTTTGCGTT	1020
GAGGGATTGG	CAGCGATGGC	TTCCAGATGG	GCTGAAACCC	TGCCCCGTATT	TATTTAAACT	1080
GGTTCCTCGT	GGAGAGCTGT	GAATCGGGCT	CTGTATGCGC	TCGAGAAAAG	CCCCATTCAT	1140

GAGAGGCAAG	GCCCAGTGGG	TCCCCCGAC	TCCCCGACCC	CCCTCTCCCA	CAATATATCC	1200
CCCCCTCCCTG	TGCCCCGCTG	CCGCCACCTC	CCGGGCTCCG	GCCCCGCGCG	CAGCGGCGAC	1260
GAAGCAACAC	AGTTCCCCGA	AAGAGGTAGC	TTTTTAATTG	GCCAGCCACA	AAGAATCACT	1320
TATGCCGCAC	GGCGGTAACG	AGGGGAACCG	GATCGGGCGG	CCAGGATGCT	ATCTGTGTAG	1380
CCCTTTTCGT	GCCACAATTA	GGGTGGTGCT	GGCTTCCTCC	GACCGCACCT	AGGCGATCTG	1440
GTTACACTGT	TGGCTCCTTT	CTTGGGCAGT	CATTTAATCC	TACTTTTAC	TCTACGAATG	1500
TCTGTCTGAT	GGAGGGCTGT	GTCCGGAGCC	CCATCCACAA	AGAGTCAGCC	AGCAGCTCTC	1560
ACACCCGGCT	GGATCTCATA	TGGTGCACCTC	TCAGTACAAT	CTGCTCTGAT	GCCGCATAGT	1620
TAAGCCAGCC	AAGCTAGCTT	GCGCAAGCTA	GCTTGCGATC	CGTAAAAATG	TGTGAGAGTT	1680
ACAAAAATGTC	TTCCGGGCTA	AGATCCGACA	GCCATGGTCC	AAAGAAGACT	TCGGCACTGC	1740
AGACTTAAAA	CCAGCTTTCT	AGCAGAGGCA	GAAGGATCTA	GAGCCAAAGG	CAAAGACTTG	1800
AATAGGCTGG	GAAGATGCAA	GAATGGCATT	TTACATAAAG	AACACTCTCT	CCTTTTCCAG	1860
CCAGCACACT	TGCATAGAAA	TTAAGTTTTA	CACCTGAAGT	TCTTTGTTTC	CATCCTGAGA	1920
AGCTCCAAAG	TCTGAGGTGG	TGTGGTATGC	TGGGTAATTC	TCCCCACCCC	CCAACATTCC	1980
CTGGGGGTTT	CATGGGGGTA	GCTTCTCCCA	AGGACTTCCA	GCGGCAACAC	AGAAATCCCA	2040
CTTCGAGACA	AAGGAGTTAC	TGCTTAAATC	AGGCCCTAAT	TTCCAAGGTT	CCCTTTGCTT	2100
AAAGTTCCCT	AGAGGACCAT	CTCACTTCTA	AAGAAAAGGT	GTATTTCGGG	ACCCATCCTC	2160
AACCTCCTTG	TTATGGAAGG	AGACTTCGGG	AACAGAGCAA	GGGCTGAGCC	TCCGGCAGTT	2220
TGGGGTAAGG	TTGGGGTTGG	GGGGAGCAAG	GAAGGCAAGT	GAGGCTGGAG	GCCCAGGGAT	2280
AGGGGAAGAT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	CTCGGGGATG	2340
GTGGTGGTGG	ACAAC TAGGA	AACTCTGGCG	CTTTCTCCTC	CCCTCACAAA	ACTGAGTCCA	2400
GCTGGAGCCG	CCTCCAGACT	CTCTGGCCAG	GGCCTCAGAG	TGGTCAACAG	TCCCTGGCCA	2460
GCGTTGCTCT	CTCCAGGCTA	AGGGCACCCA	CTCCCCTGGA	GATTCCTGAA	CCTGGGCCAG	2520
GAAGAGCCGA	ATTAGACAAG	TGTCTCCAAT	CCGGCTGCGT	GCGGATTTTG	TTGCGGTGTC	2580
CCTCGGTTGT	CTGCAGTTCC	TTTAGTCCCT	TCCCTGGCCT	GCCCCTTACA	CCTCCACACA	2640
GGTCCCCCTC	TGTGTAGGAA	TACACCAGAC	CCTCTCTTAG	CCACACACAC	CTCCAGTCCC	2700
CCGTCTACCT	AGATTTTTTT	CATAGCTAGT	TGGATGGGGG	ATGGGTTAGG	GAGGCTGGGT	2760
TTGCGAGCCT	CCAGGTGGGA	GTTCAACGAC	AGGTACTCCG	CAAAGGAGCT	GGAAGGCAGG	2820
TCTGGA AAAC	TGTCCCCCAG	ATTTAGGATT	CTGGGCAGCT	TCCATCAGCT	TATACTTTGG	2880
CTCCCCCGCC	CCCTAAACTC	CCCATCCCCA	CCTTCCTTTC	TCCCGTTACT	TCGTCCTCCC	2940
TCGCCTTTCC	AGCCTTGAGT	CTAAAGCTCC	ATGCTTATGC	CTCTGCAAAC	AACCCCTCC	3000
CTTCTAACCC	CAGCAGAACT	CCGAGGAAAG	GGGCCGGAGG	CCCCCTTCT	CGCCTGTGGT	3060
TAGAGGGGGC	AGTGTGGCAG	TCCCAAGTGG	GGGCGACCGG	AGGCCGTCTC	GGTGCCCCGC	3120
CCGATCAGGC	CACTGGGCAC	ATCGGGGGCG	GGAAGCTGGG	CTACCAAAG	GGGCGACTGG	3180
CCTTGGCAGG	TGTGGGCTCT	GGTCCGGCCT	GGGCAGGCTC	CGGGGGCGGG	GTCTCAGGTT	3240
ACAGCCCCGC	GGGGGGCTGG	GGGGCGGCCC	GCGGTTTG	CTGGTTTGCC	AGCCTTTGGA	3300
GCGACCGGGA	GCATATAACC	GGAGCCTCTG	CTGGGAGAAG	ACGCAGAGCG	CCGCTGGGCT	3360
GCCGGGTCTC	CTGCCTCCTC	CTCCTGCTCC	TAGAGCCTCC	TGCATGAGGG	CGCGGTAGAG	3420
ACCCGGACCC	GCTCCGTGCT	CTGCCGCCTC	GCCGAGCTTC	GCCC GCAAGC	TGGGGAATTC	3480
ATATGTCTAG	ATTAGATAAA	AGTAAAGTGA	TTAACAGCGC	ATTAGAGCTG	CTTAATGAGG	3540
TCGGAATCGA	AGGTTTAACA	ACCCGTAAAC	TCGCCCAGAA	GCTAGGTGTA	GAGCAGCCTA	3600
CATTGTATTG	GCATGTAAAA	AATAAGCGGG	CTTTGCTCGA	CGCCTTAGCC	ATTGAGATGT	3660
TAGATAGGCA	CCATACTCAC	TTTTGCCCTT	TAGAAGGGGA	AAGCTGGCAA	GATTTTTTAC	3720
GTAATAACGC	TAAAAGTTTT	AGATGTGCTT	TACTAAGTCA	TCGCGATGGA	GCAAAAGTAC	3780
ATTTAGGTAC	ACGGCCTACA	GAAAAACAGT	ATGAAACTCT	CGAAAATCAA	TTAGCCTTTT	3840
TATGCCAACA	AGGTTTTTCA	CTAGAGAATG	CATTATATGC	ACTCAGCGCT	GTGGGGCATT	3900
TTACTTTAGG	TTGCGTATTG	GAAGATCAAG	AGCATCAAGT	CGCTAAAGAA	GAAAGGGAAA	3960
CACCTACTAC	TGATAGTATG	CCGCCATTAT	TACGACAAGC	TATCGAATTA	TTTGATCACC	4020
AAGGTGCAGA	GCCAGCCTTC	TTATTTCGGC	TTGAATTGAT	CATATGCGGA	TTAGAAAAAC	4080
AACTTAAATG	TGAAAGTGGG	TCCGCGTACA	GCCGCGCGCG	TACGAAAAAC	AATTACGGGT	4140
CTACCATCGA	GGGCCTGCTC	GATCTCCCGG	ACGACGACGC	CCCCGAAGAG	GCGGGGCTGG	4200

CGGCTCCGCG	CCTGTCCTTT	CTCCCCGCGG	GACACACGCG	CAGACTGTCTG	ACGGCCCCCC	4260
CGACCGATGT	CAGCCTGGGG	GACGAGCTCC	ACTTAGACGG	CGAGGACGTG	GCGATGGCGC	4320
ATGCCGACGC	GCTAGACGAT	TTCGATCTGG	ACATGTTGGG	GGACGGGGAT	TCCCCGGGTC	4380
CGGGATTTAC	CCCCACGAC	TCCGCCCCCT	ACGGCGCTCT	GGATATGGCC	GACTTCGAGT	4440
TTGAGCAGAT	GTTTACCGAT	GCCCTTGGAA	TTGACGAGTA	CGGTGGGTAG	GGGGCGCGAG	4500
GATCCTCTAG	AGGGCCCTAT	TCTATAGTGT	CACCTAAATG	CTAGAGGATC	TTTGTGAAGG	4560
AACCTTACTT	CTGTGGTGTG	ACATAATTGG	ACAAACTACC	TACAGAGATT	TAAAGCTCTA	4620
AGGTAAATAT	AAAATTTTTA	AGTGTATAAT	GTGTTAAACT	ACTGATTCTA	ATTGTTTGTG	4680
TATTTTAGAT	TCCAACCTAT	GGAAGTGTG	AATGGGAGCA	GTGGTGGAA	GCCTTTAATG	4740
AGGAAAACCT	GTTTTGCTCA	GAAGAAATGC	CATCTAGTGA	TGATGAGGCT	ACTGCTGACT	4800
CTCAACATTC	TACTCCTCCA	AAAAAGAAGA	GAAAGGTAGA	AGACCCCAAG	GACTTTCCTT	4860
CAGAAATGCT	AAGTTTTTTG	AGTCATGCTG	TGTTTAGTAA	TAGAACTCTT	GCTTGCTTTG	4920
CTATTTACAC	CACAAAGGAA	AAAGCTGCAC	TGCTATACAA	GAAAATTATG	GAAAAATATT	4980
TGATGTATAG	TGCCTTGACT	AGAGATCATA	ATCAGCCATA	CCACATTTGT	AGAGGTTTTA	5040
CTTGCTTTAA	AAAACCTCCC	ACACCTCCCC	CTGAACCTGA	AACATAAAAT	GAATGCAATT	5100
GTTGTTGTTA	ACTTGTTTAT	TGCAGCTTAT	AATGGTTACA	AATAAAGCAA	TAGCATCACA	5160
AATTTACAA	ATAAAGCATT	TTTTTCACTG	CATTCTAGTT	GTGGTTTGTC	CAAACATCATC	5220
AATGTATCTT	ATCATGTCTG	GATCATCCCG	CCATGGGTAT	ACATCGATGC	GGCCGC	5276

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTACCACTA	GTAAGCTTAG	ATCCACTGTC	TGGGATTATA	TCAGGACAAC	CGAAGCCTGG	60
AAAGTGTATT	AGGTAGAGCA	TTTTCTTCCA	CGTGTTTGGG	CACGTTTCCG	ACAGCTAGGA	120
TTCCAGCTCT	GTCTTTGTAT	GTTACAGACT	GTAAATCAAT	CGCAGGTGAA	ACTGTTTGGG	180
CAGTAGGTGG	GGATCAAAGA	CCCTCCGCCC	GTGAGACTCT	AGGCGCTTTC	CCCTGCCACC	240
AGCCTGTCTC	CAGAGATGCT	CTGGAAGGAG	GCGGGCCCCG	GCGGTCTTTC	TGCTCTTTAG	300
CGTGCGCGAC	GCGGCGGCGG	GGGCAGGGCT	GGAGCAGAGA	GCGCTGCAGT	GATAGAAGTT	360
TCTGACCCCG	CTGCGCAGGG	CGGCAGGGTG	GCAGGGTGGC	AGGGTGCGCA	GCTAAGCCAG	420
AGCCGAACGC	TGGAGCTCTG	GGAGGAACAT	CGAAGTGTTT	GTATGTGGTC	TGAGATCGGC	480
CTGACTATAT	TTTTTTGTCC	TAAATTTGCA	AGCACACACC	CACAAAGCTG	CGGTCTTGAC	540
CGGTATTCTT	TATAGAGCGC	AATGGAGTGA	GCTGAGTGTC	TAAACGATTT	CCCTAATTCA	600
TCTGATAGCA	GAGGCGCTCT	CCTAATTGGC	GAAGAGCTGC	CTCATGTCCG	CAACTTTTTG	660
GCAGAGTGAA	TTCCACAGCT	TTGTGTGTGT	GTGTGGGGGG	GGGTGTAAGG	GGTGTCTAAA	720
ACTTTCGGTC	TCCTACTATT	CTGTATCTCG	ACCGGTTGGT	TTTACACCCC	GGCTCATCTC	780
ATCAACGCAA	ACACCCCCAC	TCTCCTATGG	ACCCAAGGAC	CTGACGTGGG	GGAAGGTGGA	840
CATTAGGAAT	GTCAGAAACC	TAGAGTCCAC	GCTCCTCCTC	TCCATCTTTC	CACGAGTTTG	900
GGAAACTTCT	TGGCTGCGAA	GACTTTGACC	CACATCTGCA	TTTCTCAGCC	CCAGCTTCCA	960
AAAGTGCTGC	AGGTTCGGGA	GGGGAGACCT	CAGTCCTCCT	TTGTGAGGCT	TGTTTGC GTT	1020
GAGGGATTGG	CAGCGATGGC	TTCCAGATGG	GCTGAAACCC	TGCCCCGATT	TATTTAAACT	1080
GGTTCCTCGT	GGAGAGCTGT	GAATCGGGCT	CTGTATGCGC	TCGAGAAAAG	CCCCATTCAT	1140
GAGAGGCAAG	GCCCAGTGGG	TCCCCCGAC	TCCCCGACCC	CCCTCTCCCA	CAATATATCC	1200

CCCCCTCCCTG	TGCCCCGCCTG	CCGCCACCTC	CCGGGCTCCG	GCCCCGCGCG	CAGCGGCGAC	1260
GAAGCAACAC	AGTTCCCCGA	AAGAGGTAGC	TTTTTAATTG	GCCAGCCACA	AAGAATCACT	1320
TATGCCGCAC	GGCGGTAAACG	AGGGGAACCG	GATCGGGCGG	CCAGGATGCT	ATCTGTGTAG	1380
CCCTTTTCGT	GCCACAATTA	GGGTGGTGCT	GGCTTCCTCC	GACCGCACCT	AGGCGATCTG	1440
GTTACACTGT	TGGCTCCTTT	CTTGGGCAGT	CATTTAATCC	TACTTTTTTAC	TCTACGAATG	1500
TCTGTCTGAT	GGAGGGCTGT	GTCCGGAGCC	CCATCCACAA	AGAGTCAGCC	AGCAGCTCTC	1560
ACACCCGCT	GGATCTCATA	TGGTGCACCT	TCAGTACAAT	CTGCTCTGAT	GCCGCATAGT	1620
TAAGCCAGCC	AAGCTAGCTT	GCGCAAGCTA	GCTTGCGATC	CGTAAAAATG	TGTGAGAGTT	1680
ACAAAATGTC	TTCCGGGCTA	AGATCCGACA	GCCATGGTCC	AAAGAAGACT	TCGGCACTGC	1740
AGACTTAAAA	CCAGCTTTCT	AGCAGAGGCA	GAAGGATCTA	GAGCCAAAGG	CAAAGACTTG	1800
AATAGGCTGG	GAAGATGCAA	GAATGGCATT	TTACATAAAG	AACACTCTCT	CCTTTTCCAG	1860
CCAGCACACT	TGCATAGAAA	TTAAGTTTTA	CACTTGAAAGT	TCTTTGTTTC	CATCCTGAGA	1920
AGCTCCAAAG	TCTGAGGTGG	TGTGGTATGC	TGGGTAATTC	TCCCCACCCC	CCAACATTCC	1980
CTGGGGGTTC	CATGGGGGTA	GCTTCTCCCA	AGGACTTCCA	GCGGCAACAC	AGAAATCCCA	2040
CTTCGAGACA	AAGGAGTTAC	TGCTTAAATC	AGGCCCTAAT	TTCCAAGGTT	CCCTTTGCTT	2100
AAAGTTCCCT	AGAGGACCAT	CTCACTTCTA	AAGAAAAGGT	GTATTTCGGGG	ACCCATCCTC	2160
AACCTCCTTG	TTATGGAAGG	AGACTTCGGG	AACAGAGCAA	GGGCTGAGCC	TCCGGCAGTT	2220
TGGGGTAAGG	TTGGGGTTGG	GGGGAGCAAG	GAAGGCAAGT	GAGGCTGGAG	GCCCAGGGAT	2280
AGGGGAAGAT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	CTCGGGGATG	2340
GTGGTGGTGG	ACAAC TAGGA	AACTCTGGCG	CTTTCTCCTC	CCCTCACAAA	ACTGAGTCCA	2400
GCTGGAGCCG	CCTCCAGACT	CTCTGGCCAG	GGCCTCAGAG	TGGTCAACAG	TCCCTGGCCA	2460
GCGTTGCTCT	CTCCAGGCTA	AGGGCACCCA	CTCCCCTGGA	GATTCCTGAA	CCTGGGCCAG	2520
GAAGAGCCGA	ATTAGACAAG	TGTCTCCAAT	CCGGCTGCGT	GCGGATTTTG	TTGCGGTGTC	2580
GCTCGGTTGT	CTGCAGTTCC	TTTAGTCCCT	TCCCTGGCCT	GCCCCTTACA	CCTCCACACA	2640
GGTCCCCCTC	TGTGTAGGAA	TACACCAGAC	CCTCTCTTAG	CCACACACAC	CTCCAGTCCC	2700
CGTCTACCT	AGATTTTTTT	CATAGCTAGT	TGGATGGGGG	ATGGGTTAGG	GAGGCTGGGT	2760
TTGCGAGCCT	CCAGGTGGGA	GTTCAACGAC	AGGTACTCCG	CAAAGGAGCT	GGAAGGCAGG	2820
TCTGAAAAAC	TGTCCCCCAG	ATTTAGGATT	CTGGGCAGCT	TCCATCAGCT	TATACTTTGG	2880
CTCCCCCGCC	CCCTAAACTC	CCCATCCCCA	CCTTCCTTTC	TCCCGTTACT	TCGTCCTCCC	2940
TCGCCTTTCC	AGCCTTGAGT	CTAAAGCTCC	ATGCTTATGC	CTCTGCAAAC	AACCCCTCC	3000
CTTCTAACCC	CAGCAGAACT	CCGAGGAAAG	GGGCCGGAGG	CCCCCCTTCT	CGCCTGTGGT	3060
TAGAGGGGGC	AGTGTGGCAG	TCCCAAGTGG	GGGCGACCGG	AGGCCGTCTC	GGTGCCCCGC	3120
CCGATCAGGC	CACTGGGCAC	ATCGGGGGCG	GGAAGCTGGG	CTCACCAAAG	GGGCGACTGG	3180
CCTTGGCAGG	TGTGGGCTCT	GGTCCGGCCT	GGGCAGGCTC	CGGGGGCGGG	GTCTCAGGTT	3240
ACAGCCCCGC	GGGGGGCTGG	GGGGCGGCCC	GCGGTTTGCC	CTGGTTTGCC	AGCCTTTGGA	3300
GCGACCGGGA	GCATATAACC	GGAGCCTCTG	CTGGGAGAAG	ACGCAGAGCG	CCGCTGGGCT	3360
GCCGGGTCTC	CTGCCTCCTC	CTCCTGCTCC	TAGAGCCTCC	TGCATGAGGG	CGCGGTAGAG	3420
ACCCGGACCC	GCTCCGTGCT	CTGCCGCCTC	GCCGAGCTTC	GCCCGCAAGC	TGGGGAATTC	3480
GGATCCCCGG	GATCGAAAGA	GCCTGCTAAA	GCAAAAAAGA	AGTCACCATG	TCGTTTACTT	3540
TGACCAACAA	GAACGTGATT	TTCGTTGCCG	GTCTGGGAGG	CATTGGTCTG	GACACCAGCA	3600
AGGAGCTGCT	CAAGCGCGAT	CCCGTCGTTT	TACAACGTCG	TGACTGGGAA	AACCCTGGCG	3660
TTACCCAACT	TAATCGCCTT	GCAGCACATC	CCCCTTTCGC	CAGCTGGCTT	TATAGCGAAG	3720
AGGCCCGCAC	CGATCGCCCT	TCCCAACAGT	TGCGCAGCCT	GAATGGCGAA	TGGCGCTTTG	3780
CCTGGTTTCC	GGCACCAGAA	GCGGTGCCGG	AAAGCTGGCT	GGAGTGCGAT	CTTCCTGAGG	3840
CCGATACTGT	CGTCGTCCCC	TCAAAC TGGC	AGATGCACGG	TTACGATGCG	CCCATCTACA	3900
CCAACGTAAC	CTATTCCATT	ACGGTCAATC	CGCCGTTTGT	TCCCACGGAG	AATCCGACGG	3960
GTTGTTACTC	GCTCACATTT	AATGTTGATG	AAAGCTGGCT	ACAGGAAGGC	CAGACGCGAA	4020
TTATTTTTGA	TGGCGTTAAC	TTGGCGTTTC	ATCTGTGGTG	CAACGTGCGC	TGGGTCGGTT	4080
ACGGCCAGGA	CAGTCGTTTG	CCGTCTGAAT	TTGACCTGAG	CGCATTTTTA	CGCGCCGGAG	4140
AAAACCGCCT	CGCGGTGATG	GTGCTGCGTT	GGAGTGACGG	CAGTTATCTG	GAAGATCAGG	4200
ATATGTGGCG	GATGAGCGGC	ATTTTCCGTG	ACGTCTCGTT	GCTGCATAAA	CCGACTACAC	4260

AAATCAGCGA	TTTCCATGTT	GCCACTCGCT	TTAATGATGA	TTTCAGCCGC	GCTGAACTGG	4320
AGGCTGAAGT	TCAGATGTGC	GGCGAGTTGC	GTGACTACCT	ACGGGTAACA	GTTTCTTTAT	4380
GGCAGGGTGA	AACGCAGGTC	GCCAGCGGCA	CCGCGCCTTT	CGGCGGTGAA	ATTATCGATG	4440
AGCGTGGTGG	TTATGCCGAT	CGCGTCACAC	TACGTCTGAA	CGTCGAAAAC	CCGAAACTGT	4500
GGAGCGCCGA	AATCCCGAAT	CTCTATCGTG	CGGTGGTTGA	ACTGCACACC	GCCGACGGCA	4560
CGCTGATTGA	AGCAGAAGCC	TGCGATGTGC	GTTTCCGCGA	GGTGCGGATT	GAAAATGGTC	4620
TGCTGCTGCT	GAACGGCAAG	CCGTTGCTGA	TTCGAGGCGT	TAACCGTCAC	GAGCATCATC	4680
CTCTGCATGG	TCAGGTCATG	GATGAGCAGA	CGATGGTGCA	GGATATCCTG	CTGATGAAGC	4740
AGAACAACCT	TAACGCCGTG	CGCTGTTTCG	ATTATCCGAA	CCATCCGCTG	TGGTACACGC	4800
TGTGCGACCG	CTACGGCCTG	TATGTGGTGG	ATGAAGCCAA	TATTGAAACC	CACGGCATGG	4860
TGCCAATGAA	TCTGCTGACC	GATGATCCGC	GCTGGCTACC	GGCGATGAGC	GAACGCGTAA	4920
CGCGAATGGT	GCAGCGCGAT	CGTAATCACC	CGAGTGTGAT	CATCTGGTCG	CTGGGGAATG	4980
AATCAGGCCA	CGGCGCTAAT	CACGACGCGC	TGTATCGCTG	GATCAAATCT	GTCGATCCTT	5040
CCCGCCCGGT	GCAGTATGAA	GGCGGCGGAG	CCGACACCAC	GGCCACCGAT	ATTATTTGCC	5100
CGATGTACGC	GCGCGTGGAT	GAAGACCAGC	CCTTCCCGGC	TGTGCCGAAA	TGGTCCATCA	5160
AAAAATGGCT	TTCGCTACCT	GGAGAGACGC	GCCCCGCTGAT	CCTTTGCGAA	TACGCCCACG	5220
CGATGGGTAA	CAGTCTTGGC	GGTTTCGCTA	AATACTGGCA	GGCGTTTCGT	CAGTATCCCC	5280
GTTTACAGGG	CGGCTTTCGTC	TGGGACTGGG	TGGATCAGTC	GCTGATTAAA	TATGATGAAA	5340
ACGGCAACCC	GTGGTCGGCT	TACGGCGGTG	ATTTTGGCGA	TACGCCGAAC	CATCGCCAGT	5400
TCTGTATGAA	CGGTCTGGTC	TTTGCCGACC	GCACGCCGCA	TCCAGCGCTG	ACGGAAGCAA	5460
AACACCAGCA	GCAGTTTTTC	CAGTTCCGTT	TATCCGGGCA	AACCATCGAA	GTGACCAGCG	5520
AATACCTGTT	CCGTCATAGC	GATAACGAGC	TCCTGCACTG	GATGGTGGCG	CTGGATGGTA	5580
AGCCGCTGGC	AAGCGGTGAA	GTGCCCTCTGG	ATGTCGCTCC	ACAAGGTAAA	CAGTTGATTG	5640
AACTGCCTGA	ACTACCGCAG	CCGGAGAGCG	CCGGGCAACT	CTGGCTCACA	GTACGCGTAG	5700
TGCAACCGAA	CGCGACCGGA	TGGTCAGAAG	CCGGGCACAT	CAGCGCCTGG	CAGCAGTGGC	5760
GTCTGGCGGA	AAACCTCAGT	GTGACGCTCC	CCGCCGCGTC	CCACGCCATC	CCGCATCTGA	5820
CCACCAGCGA	AATGGATTTT	TGCATCGAGC	TGGGTAAATA	GCGTTGGCAA	TTTAACCGCC	5880
AGTCAGGCTT	TCTTTCACAG	CTGTGGATTG	GCGATAAAAA	ACAACCTGCTG	ACGCCGCTGC	5940
GCGATCAGTT	CACCCGTGCA	CCGCTGGATA	ACGACATTGG	CGTAAGTGAA	GCGACCCGCA	6000
TTGACCCTAA	CGCCTGGGTC	GAACGCTGGA	AGGCGGCGGG	CCATTACCAG	GCCGAAGCAG	6060
CGTTGTGTGCA	GTGCACGGCA	GATACACTTG	CTGATGCGGT	GCTGATTACG	ACCGCTCACG	6120
CGTGGCAGCA	TCAGGGGAAA	ACCTTATTTA	TCAGCCGGAA	AACCTACCGG	ATTGATGGTA	6180
GTGGTCAAAT	GGCGATTACC	GTTGATGTTG	AAGTGGCGAG	CGATACACCG	CATCCGGCGC	6240
GGATTGGCCT	GAAC TGCCAG	CTGGCGCAGG	TAGCAGAGCG	GGTAAACTGG	CTCGGATTAG	6300
GGCCGCAAGA	AAACTATCCC	GACCGCCTTA	CTGCCGCTTG	TTTTGACCGC	TGGGATCTGC	6360
CATTGTCAGA	CATGTATACC	CCGTACGTCT	TCCCGAGCGA	AAACGGTCTG	CGCTGCGGGA	6420
CGCGCGAATT	GAATTATGGC	CCACACCAGT	GGCGCGGCGA	CTTCCAGTTC	AACATCAGCC	6480
GCTACAGTCA	ACAGCAACTG	ATGGAAACCA	GCCATCGCCA	TCTGCTGCAC	GCGGAAGAAG	6540
GCACATGGCT	GAATATCGAC	GGTTTCCATA	TGGGGATTGG	TGGCGACGAC	TCCTGGAGCC	6600
CGTCAGTATC	GGCGGAATTA	CAGCTGAGCG	CCGGTCGCTA	CCATTACCAG	TTGGTCTGGT	6660
GTCAAAAATA	ATAATAACCG	GCAGGCCATG	TCTGAAAGTA	TTCGCGTAAG	GAAATCCATT	6720
ATGTACTATT	TAAAAAACAC	AAACTTTTGG	ATGTTTCGGTT	TATTCTTTTT	CTTTTACTTT	6780
TTTATCATGG	GAGCCTACTT	CCCGTTTTTC	CCGATTGGGC	TACATGACAT	CAACCATATG	6840
AGCAAAAGTG	ATACGGGTAT	TATTTTTGCC	GCTATTTCTC	TGTTGTCGCT	ATTATTCCAA	6900
CCGCTGTTGG	TCTGCTTTCT	GACAAACTCG	GCCTCGACTC	TAGACTGAGA	ACTTCAGGGT	6960
GAGTTTGGGG	ACCCTTGATT	GTTCTTTCTT	TTTCGCTATT	GAAAAATTCA	TGTTATATGG	7020
AGGGGGCAAA	GTTTTTCAGGG	TGTTGTTTAG	AATGGGAAGA	TGTCCCTTGT	ATCACCATGG	7080
ACCCTCATGA	TAATTTTGTT	TCTTTCACCT	TCTACTCTGT	TGACAACCAT	TGTCTCCTCT	7140
TATTTTCTTT	TCATTTTCTG	TAAC TTTTTT	CGTTAAACTT	TAGCTTGCAT	TTGTAACGAA	7200
TTTTTAAATT	CAC TTTCTGTT	TATTTGTCAG	ATTGTAAGTA	CTTTCTCTAA	TCACTTTTTT	7260
TTCAAGGCAA	TCAGGGTAAT	TATATTGTAC	TTCAGCACAG	TTTTAGAGAA	CAATTGTTAT	7320

AATTAAATGA	TAAGGTAGAA	TATTTCTGCA	TATAAATTCT	GGCTGGCGTG	GAAATATTCT	7380
TATTGGTAGA	AACAAC TACA	TCCTGGTAAT	CATCCTGCCT	TTCTCTTTAT	GGTTACAATG	7440
ATATACACTG	TTTGAGATGA	GGATAAAATA	CTCTGAGTCC	AAACCGGGCC	CCTCTGCTAA	7500
CCATGTTTCA	TGCCTTCTTCT	TTTTCCTACA	GCTCCTGGGC	AACGTGCTGG	TTGTTGTGCT	7560
GTCTCATCAT	TTTGGCAAAG	AATTCACTCC	TCAGGTGCAG	GCTGCCTATC	AGAAGGTGGT	7620
GGCTGGTGTG	GCCAATGCCC	TGGCTCACAA	ATACCACTGA	GATC		7664

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGAGGGCCTG CTCGATCTCC 20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCATTCCAC CACTGCTCCC 20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCACCTT CTCATGACCT C 21

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTGGTGTAG ATGGGCGCAT CG

22

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGGGGTCTC AGGTTACAGC C

21

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCTCTGGC CTGCTGGCTC ATG

23

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAGGAGAGTC TTGCCTGTAT CCTC

24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAAGATGCAT	CCAGGGGTCC	TGGCTGCCTT	CCTCTTCTTG	AGCTGGACTC	ATTGTCGGGC	60
CCTGCCCCTT	CCCAGTGGTG	GTGATGAAGA	TGATTTGTCT	GAGGAAGACC	TCCAGTTTGC	120
AGAGCGCTAC	CTGAGATCAT	ACTACCATCC	TACAAATCTC	GCGGGAATCC	TGAAGGAGAA	180
TGCAGCAAGC	TCCATGACTG	AGAGGCTCCG	AGAAATGCAG	TCTTTCTTCG	GCTTAGAGGT	240
GACTGGCAAA	CTTGACGATA	ACACCTTAGA	TGTCATGAAA	AAGCCAAGAT	GCGGGGTTGT	300
CGATGTGGG	TGAATACAATG	TTTTCCCTCG	AACTCTTAAA	TGGTCCAAAA	TGAATTTAAC	360
CTACAGAATT	TGAATTACA	CCCCTGATAT	GACTCATTCT	GAAGTCGAAA	AGGCATTCAA	420
AAAAGCCTTC	AAAGTTTGGT	CCGATGTAAC	TCCTCTGAAT	TTTACCAGAC	TTACGATGG	480
CATTGCTGAC	ATCATGATCT	CTTTTGGAA	TAAGGAGCAT	GGCGACTTCT	ACCCATTTGA	540
TGGGCCCTCT	GGCCTGCTGG	CTCATGCTTT	TCCTCCTGGG	CCAAATTATG	GAGGAGATGC	600
GCATTTTGAT	GATGATGAAA	CCTGGACAAG	TAGTTCCAAA	GGCTACAAC	TGTTTCTTGT	660
TGCTGCGCAT	GAGTTCGGCC	ACTCCTTAGG	TCTTGACCAC	TCCAAGGACC	CTGGAGCACT	720
CATGTTTCCT	ATCTACACCT	ACACCGGCAA	AAGCCACTTT	ATGCTTCCTG	ATGACGATGT	780
ACAAGGGATC	CAGTCTCTCT	ATGGTCCAGG	AGATGAAGAC	CCCAACCCTA	AACATCCAAA	840
AACGCCAGAC	AAATGTGACC	CTTCCTTATC	CCTTGATGCC	ATTACCAGTC	TCCGAGGAGA	900
AACAATGATC	TTTAAAGACA	GATTCTTCTG	GCGCCTGCAT	CCTCAGCAGG	TTGATGCGGA	960
GCTGTTTTTA	ACGAAATCAT	TTTGGCCAGA	ACTTCCCAAC	CGTATTGATG	CTGCATATGA	1020
GCACCTTCT	CATGACCTCA	TCTTCATCTT	CAGAGGTAGA	AAATTTTGGG	CTCTTAATGG	1080
TTATGACATT	CTGGAAGGTT	ATCCCAAAAA	AATATCTGAA	CTGGGTCTTC	CAAAGAAGT	1140
TAAGAAGATA	AGTGCAGCTG	TTCACCTTGA	GGATACAGGC	AAGACTCTCC	TGTTCTCAGG	1200
AAACCAGGTC	TGGAGATATG	ATGATACTAA	CCATATTATG	GATAAAGACT	ATCCGAGACT	1260
AATAGAAGAA	GACTTCCCAG	GAATTGGTGA	TAAAGTAGAT	GCTGTCTATG	AGAAAAATGG	1320
TTATATCTAT	TTTTTCAACG	GACCCATACA	GTTTGAATAC	AGCATCTGGA	GTAACCGTAT	1380
TGTTTCGCGTC	ATGCCAGCAA	ATTCCATTTT	GTGGTGTAA	GTGTCTTTTT	AAAAATTGTT	1440
ATTTAAATCC	TGAAGAGCAT	TTGGGGTAAT	ACTTCCAGAA	GTGCGGGGTA	GGGGAAGAAG	1500
AGCTATCAGG	AGAAAGCTTG	G				1521

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Arg Cys Gly Xaa Pro Asp

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

His Glu Xaa Gly His Xaa Xaa Xaa Xaa Xaa His Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met His Pro Gly Val Leu Ala Ala Phe Leu Phe Leu Ser Trp Thr His
 1 5 10 15
 Cys Arg Ala Leu Pro Leu Pro Ser Gly Gly Asp Glu Asp Asp Leu Ser
 20 25 30
 Glu Glu Asp Leu Gln Phe Ala Glu Arg Tyr Leu Arg Ser Tyr Tyr His
 35 40 45
 Pro Thr Asn Leu Ala Gly Ile Leu Lys Glu Asn Ala Ala Ser Ser Met
 50 55 60
 Thr Glu Arg Leu Arg Glu Met Gln Ser Phe Phe Gly Leu Glu Val Thr
 65 70 75 80
 Gly Lys Leu Asp Asp Asn Thr Leu Asp Val Met Lys Lys Pro Arg Cys
 85 90 95
 Gly Gly Val Asp Val Gly Glu Tyr Asn Val Phe Pro Arg Thr Leu Lys
 100 105 110
 Trp Ser Lys Met Asn Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp
 115 120 125
 Met Thr His Ser Glu Val Glu Lys Ala Phe Lys Lys Ala Phe Lys Val
 130 135 140
 Trp Ser Asp Val Thr Pro Leu Asn Phe Thr Arg Leu His Asp Gly Ile
 145 150 155 160
 Ala Asp Ile Met Ile Ser Phe Gly Ile Lys Glu His Gly Asp Phe Tyr

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